

SEQUENCE LISTING

<110> TOMLINSON, Stephen
HOLERS, V. Michael

<120> Complement Receptor 2 Targeted
Complement Modulators

<130> 577712000200

<140> US 10/534,772
<141> 2003-11-13

<150> PCT/US2003/036459
<151> 2003-11-13

<150> US 60/426,676
<151> 2002-11-15

<160> 29

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 1041
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 1
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tttcccgagg atactgtaat aacgtacaaa tgtgaagaaa gctttgtgaa aattcctggc 120
gagaaggact cagtgatctg ccttaaggcc agtcaatggt cagatattga agagttctgc 180
aatcgttagct gcgaggtgcc aacaaggcta aattctgcat ccctcaaaca gccttatatac 240
actcagaatt atttccagt cggtactgtt gtggaaatatg agtgcgcgtcc aggttacaga 300
agagaacctt ctctatcacc aaaactaact tgccttcaga atttaaaatg gtccacagca 360
gtcgaatttt gtaaaaagaa atcatgcctt aatccgggag aaatacggaa tggtcagatt 420
gatgtaccag gtggcatatt atttggtca accatctcct tctcatgtaa cacagggtac 480
aaattatttg gctcgacttc tagttttgtt cttatttcag gcagctctgt ccagtggagt 540
gaccgcgtgc cagagtgcag agaaatttat tgtccagcac caccacaaat tgacaatgga 600
ataattcaag gggAACGTGA ccattatgga tatagacagt ctgtaacgtt tgcatgtat 660
aaaggattca ccatgattgg agagcactt atttattgtt ctgtgaataa tgatgaagga 720
gagttggatgt gcccaccacc tgaatgcaga ggaaaatctc taacttccaa ggtcccacca 780
acagttcaga aacctaccac agtaaatgtt ccaactacag aagtctcacc aacttctcag 840
aaaaccacca caaaaaccac cacaccaat gctcaagcaa cacggagttac acctgtttcc 900
aggacaacca agcattttca tggaaacaacc ccaaataaaag gaagtggAAC cacttcaggt 960
actaccgcgc ttctatctgg gcacacgtgt ttcacgttga caggtttgct tgggacgcta 1020
gtaaccatgg gcttgctgac t 1041

<210> 2
<211> 380
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 2

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Glu	Leu	Pro	Arg	Leu	Leu	Leu	Leu	Val	Leu	Leu	Cys	Leu	Pro	Ala	Val
															20
Trp	Asp	Cys	Gly	Leu	Pro	Pro	Asp	Val	Pro	Asn	Ala	Gln	Pro	Ala	Leu
															35
Glu	Gly	Arg	Thr	Ser	Phe	Pro	Glu	Asp	Thr	Val	Ile	Thr	Tyr	Lys	Cys
															50
Glu	Glu	Ser	Phe	Val	Lys	Ile	Pro	Gly	Glu	Lys	Asp	Ser	Val	Ile	Cys
															65
Leu	Lys	Gly	Ser	Gln	Trp	Ser	Asp	Ile	Glu	Glu	Phe	Cys	Asn	Arg	Ser
															85
Cys	Glu	Val	Pro	Thr	Arg	Leu	Asn	Ser	Ala	Ser	Leu	Lys	Gln	Pro	Tyr
															100
Ile	Thr	Gln	Asn	Tyr	Phe	Pro	Val	Gly	Thr	Val	Val	Glu	Tyr	Glu	Cys
															115
Arg	Pro	Gly	Tyr	Arg	Arg	Glu	Pro	Ser	Leu	Ser	Pro	Lys	Leu	Thr	Cys
															130
Leu	Gln	Asn	Leu	Lys	Trp	Ser	Thr	Ala	Val	Glu	Phe	Cys	Lys	Lys	Lys
															145
Ser	Cys	Pro	Asn	Pro	Gly	Glu	Ile	Arg	Asn	Gly	Gln	Ile	Asp	Val	Pro
															165
Gly	Gly	Ile	Leu	Phe	Gly	Ala	Thr	Ile	Ser	Phe	Ser	Cys	Asn	Thr	Gly
															180
Tyr	Lys	Leu	Phe	Gly	Ser	Thr	Ser	Ser	Phe	Cys	Leu	Ile	Ser	Gly	Ser
															195
Ser	Val	Gln	Trp	Ser	Asp	Pro	Leu	Pro	Glu	Cys	Arg	Glu	Ile	Tyr	Cys
															210
Pro	Ala	Pro	Pro	Gln	Ile	Asp	Asn	Gly	Ile	Ile	Gln	Gly	Glu	Arg	Asp
															225
His	Tyr	Tyr	Arg	Gln	Ser	Val	Thr	Tyr	Ala	Cys	Asn	Lys	Gly	Phe	
															245
Thr	Met	Ile	Gly	Glu	His	Ser	Ile	Tyr	Cys	Thr	Val	Asn	Asn	Asp	Glu
															260
Gly	Glu	Trp	Ser	Gly	Pro	Pro	Glu	Cys	Arg	Gly	Lys	Ser	Leu	Thr	
															275
Ser	Lys	Val	Pro	Pro	Thr	Val	Gln	Lys	Pro	Thr	Thr	Val	Asn	Val	Pro
															290
Thr	Thr	Glu	Val	Ser	Pro	Thr	Ser	Gln	Lys	Thr	Thr	Thr	Lys	Thr	Thr
															305
Thr	Pro	Asn	Ala	Gln	Ala	Thr	Arg	Ser	Thr	Pro	Val	Ser	Arg	Thr	Thr
															325
Lys	His	Phe	His	Glu	Thr	Thr	Pro	Asn	Lys	Gly	Ser	Gly	Thr	Thr	Ser
															340
Gly	Thr	Thr	Arg	Leu	Leu	Ser	Gly	His	Thr	Cys	Phe	Thr	Leu	Thr	Gly
															355
Leu	Leu	Gly	Thr	Leu	Val	Thr	Met	Gly	Leu	Leu	Thr				
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															380

<210> 3
<211> 306
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 3
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gattttgatg cgtgtctcat taccaaagct gggttacaag tgtataacaa gtgttggaaag 120
ttttagcatt gcaatttcaa cgacgtcaca acccgcttga gggaaaaatga gctaacgtac 180
tactgctgca agaaggacct gtgttaactt aacgaacagc ttgaaaatgg tgggacatcc 240
ttatcagaga aaacagttct tctgctggtg actccatttc tggcagcagc ctggagcctt 300
catccc 306

<210> 4
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 4
Met Gly Ile Gln Gly Gly Ser Val Leu Phe Gly Leu Leu Leu Val Leu
1 5 10 15
Ala Val Phe Cys His Ser Gly His Gln Cys Tyr Asn Cys Pro Asn Pro
20 25 30
Thr Ala Asp Cys Lys Thr Ala Val Asn Cys Ser Ser Asp Phe Asp Ala
35 40 45
Cys Leu Ile Thr Lys Ala Gly Leu Gln Val Tyr Asn Lys Cys Trp Lys
50 55 60
Phe Glu His Cys Asn Phe Asn Asp Val Thr Thr Arg Leu Arg Glu Asn
65 70 75 80
Glu Leu Thr Tyr Tyr Cys Cys Lys Lys Asp Leu Cys Asn Phe Asn Glu
85 90 95
Gln Leu Glu Asn Gly Gly Thr Ser Leu Ser Glu Lys Thr Val Leu Leu
100 105 110
Leu Val Thr Pro Phe Leu Ala Ala Trp Ser Leu His Pro
115 120 125

<210> 5
<211> 1485
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 5
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attgctgttg gtaccgtat aaggtagt tgttcaggtt ccttccgcct cattggagaa 120
aaaagtctat tatgcataac taaagacaaa gtggatggaa cctgggataaa acctgctcct 180
aaatgtgaat attcaataa atattctct tgccttgagc ccatagttacc aggaggatac 240
aaaatttagag gctctacacc ctacagacat ggtgattctg tgacatttc ctgtaaaacc 300
aacttctcca tgaacggaaa caagtctgtt tgggtcaag caaataatat gtggggccg 360
acacgactac caacctgtgt aagtgtttc cctctcgagt gtccagcact tcctatgatc 420
cacaatggac atcacacaag tgagaatgtt ggctccattt ctccaggatt gtctgtgact 480
tacagctgtg aatctggta cttgcttgtt ggagaaaaga tcattaactg tttgtcttcg 540
ggaaaatgga gtgtgtccc cccccacatgt gaagaggcac gctgtaaatc tctaggacga 600
tttcccaatg ggaaggtaaa ggagcctcca attctccggg ttgggttaac tgcaaactt 660
ttctgtatg aagggtatcg actgcaaggc ccaccttcta gtcgggtgtt aattgtgtt 720
cagggagttt cttggaccaa aatgccagta tgggtgggtt gggtgggtgg cggcggatcc 780
gactgtggcc ttcccccaga tggtaat gcccagccag ctttggaaagg ccgtacaatg 840
tttcccgagg atactgtat aacgtacaaa tggtaagaaa gctttgtgaa aattcctggc 900

gagaaggact cagtcatcg ccttaaggc agtcaatggc cagatattga agagttctgc 960
 aatcgtagct gcgagggtcc aacaaggcta aattctgcat ccctcaaaca gccttatatac 1020
 actcagaatt atttccagt cggtaactgtt gtggaatatg agtgcctgtcc aggttacaga 1080
 agagaacctt ctctatcacc aaaactaact tgccttcaga atttaaaatg gtccacagca 1140
 gtcgaatttt gtaaaaagaa atcatgcct aatccgggag aaatacggaaa tggtcagatt 1200
 gatgtaccag gtggcatatt atttggcga accatctct tctcatgtaa cacagggtac 1260
 aaattatttg gctcgacttc tagttttgt cttatccag gcagctctgt ccagtgaggt 1320
 gaccgttgc cagagtgcag agaaatttat tgtccagcac caccacaaat tgacaatgg 1380
 ataattcaag gggAACGTGA ccattatgg tatagacagt ctgtAACGTA tgcatgtat 1440
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<210> 6

<211> 495

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 6

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Tyr	Ser	Thr	Pro	Ile	Ala	Val	Gly	Thr	Val	Ile	Arg	Tyr	Ser	Cys	Ser
								20			25			30	
Gly	Thr	Phe	Arg	Leu	Ile	Gly	Glu	Lys	Ser	Leu	Leu	Cys	Ile	Thr	Lys
								35			40			45	
Asp	Lys	Val	Asp	Gly	Thr	Trp	Asp	Lys	Pro	Ala	Pro	Lys	Cys	Glu	Tyr
								50			55			60	
Phe	Asn	Lys	Tyr	Ser	Ser	Cys	Pro	Glu	Pro	Ile	Val	Pro	Gly	Gly	Tyr
								65			70			75	
Lys	Ile	Arg	Gly	Ser	Thr	Pro	Tyr	Arg	His	Gly	Asp	Ser	Val	Thr	Phe
								85			90			95	
Ala	Cys	Lys	Thr	Asn	Phe	Ser	Met	Asn	Gly	Asn	Lys	Ser	Val	Trp	Cys
								100			105			110	
Gln	Ala	Asn	Asn	Met	Trp	Gly	Pro	Thr	Arg	Leu	Pro	Thr	Cys	Val	Ser
								115			120			125	
Val	Phe	Pro	Leu	Glu	Cys	Pro	Ala	Leu	Pro	Met	Ile	His	Asn	Gly	His
								130			135			140	
His	Thr	Ser	Glu	Asn	Val	Gly	Ser	Ile	Ala	Pro	Gly	Leu	Ser	Val	Thr
								145			150			155	
Tyr	Ser	Cys	Glu	Ser	Gly	Tyr	Leu	Leu	Val	Gly	Glu	Lys	Ile	Ile	Asn
								165			170			175	
Cys	Leu	Ser	Ser	Gly	Lys	Trp	Ser	Ala	Val	Pro	Pro	Thr	Cys	Glu	Glu
								180			185			190	
Ala	Arg	Cys	Lys	Ser	Leu	Gly	Arg	Phe	Pro	Asn	Gly	Lys	Val	Lys	Glu
								195			200			205	
Pro	Pro	Ile	Leu	Arg	Val	Gly	Val	Thr	Ala	Asn	Phe	Phe	Cys	Asp	Glu
								210			215			220	
Gly	Tyr	Arg	Leu	Gln	Gly	Pro	Pro	Ser	Ser	Arg	Cys	Val	Ile	Ala	Gly
								225			230			235	
Gln	Gly	Val	Ala	Trp	Thr	Lys	Met	Pro	Val	Cys	Gly	Gly	Ser	Gly	
								245			250			255	
Gly	Gly	Gly	Ser	Asp	Cys	Gly	Leu	Pro	Pro	Asp	Val	Pro	Asn	Ala	Gln
								260			265			270	
Pro	Ala	Leu	Glu	Gly	Arg	Thr	Ser	Phe	Pro	Glu	Asp	Thr	Val	Ile	Thr
								275			280			285	
Tyr	Lys	Cys	Glu	Glu	Ser	Phe	Val	Lys	Ile	Pro	Gly	Glu	Lys	Asp	Ser
								290			295			300	
Val	Ile	Cys	Leu	Lys	Gly	Ser	Gln	Trp	Ser	Asp	Ile	Glu	Glu	Phe	Cys
								305			310			315	
															320

Asn	Arg	Ser	Cys	Glu	Val	Pro	Thr	Arg	Leu	Asn	Ser	Ala	Ser	Leu	Lys
				325				330						335	
Gln	Pro	Tyr	Ile	Thr	Gln	Asn	Tyr	Phe	Pro	Val	Gly	Thr	Val	Val	Glu
				340				345						350	
Tyr	Glu	Cys	Arg	Pro	Gly	Tyr	Arg	Arg	Glu	Pro	Ser	Leu	Ser	Pro	Lys
				355				360						365	
Leu	Thr	Cys	Leu	Gln	Asn	Leu	Lys	Trp	Ser	Thr	Ala	Val	Glu	Phe	Cys
				370				375						380	
Lys	Lys	Lys	Ser	Cys	Pro	Asn	Pro	Gly	Glu	Ile	Arg	Asn	Gly	Gln	Ile
				385				390						400	
Asp	Val	Pro	Gly	Gly	Ile	Leu	Phe	Gly	Ala	Thr	Ile	Ser	Phe	Ser	Cys
				405				410						415	
Asn	Thr	Gly	Tyr	Lys	Leu	Phe	Gly	Ser	Thr	Ser	Ser	Phe	Cys	Leu	Ile
				420				425						430	
Ser	Gly	Ser	Ser	Val	Gln	Trp	Ser	Asp	Pro	Leu	Pro	Glu	Cys	Arg	Glu
				435				440						445	
Ile	Tyr	Cys	Pro	Ala	Pro	Pro	Gln	Ile	Asp	Asn	Gly	Ile	Ile	Gln	Gly
				450				455						460	
Glu	Arg	Asp	His	Tyr	Gly	Tyr	Arg	Gln	Ser	Val	Thr	Tyr	Ala	Cys	Asn
				465				470						475	
Lys	Gly	Phe	Thr	Met	Ile	Gly	Glu	His	Ser	Ile	Tyr	Cys	Thr	Val	
				485				490						495	

<210> 7
<211> 1002
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 7
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aaaagtctat tatgcataac taaagacaaa gtggatggaa cctgggataaa acctgctcct 180
aaatgtaat attcaataa atattctct tgccttgagc ccatagttacc aggaggatac 240
aaaatttagag gctctacacc ctacagacat ggtgattctg tgacatttgc ctgtaaaaacc 300
aacttctcca tgaacggaaa caagtctgtt tgggtgtcaag caaataatat gtgggggcccc 360
acacgactac caacctgtgt aagtgttttc cctctcgagt gtccagcact tcctatgatc 420
cacaatggac atcacacaag tgagaatgtt ggctccatttgc ctccaggatt gtctgtgact 480
tacagctgttgc aatctgttta cttgttttttggagaaaatgc tcattaactg tttgtcttcg 540
ggaaaaatggaa gtgtgttccc ccccacatgt gaagaggcac gctgtaaaatc tctaggacga 600
tttcccaatg ggaaggtaaa ggagcctcca attctccggg ttgggtgttaac tgcaaacttt 660
ttctgtatg aagggtatcg actgcaaggc ccaccttcta gtcgggtgtt aattgtgttgc 720
cagggagtttgc cttggaccaa aatgccatgt tgttcaggag gaggaggatc cctgcagtgc 780
tacaactgttgc ctaacccaaatgc tgcgtactgc aaaacagccg tcaatttttc atctgatgtt 840
gatgcgtgtc tcattaccaa agctgggttca aagttgtata acaagttgttgc gaagtttgc 900
cattgcaatt tcaacgacgt cacaaccgc ttgagggaaa atgagctaac gtactactgc 960
tgcaagaagg acctgtgtaa cttaacgaa cagcttgaaa at 1002

<210> 8
<211> 334
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 8

Ile	Ser	Cys	Gly	Ser	Pro	Pro	Pro	Ile	Leu	Asn	Gly	Arg	Ile	Ser	Tyr	
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Tyr	Ser	Thr	Pro	Ile	Ala	Val	Gly	Thr	Val	Ile	Arg	Tyr	Ser	Cys	Ser	
			20					25					30			
Gly	Thr	Phe	Arg	Leu	Ile	Gly	Glu	Lys	Ser	Leu	Leu	Cys	Ile	Thr	Lys	
			35				40					45				
Asp	Lys	Val	Asp	Gly	Thr	Trp	Asp	Lys	Pro	Ala	Pro	Lys	Cys	Glu	Tyr	
			50				55					60				
Phe	Asn	Lys	Tyr	Ser	Ser	Cys	Pro	Glu	Pro	Ile	Val	Pro	Gly	Gly	Tyr	
			65				70					75			80	
Lys	Ile	Arg	Gly	Ser	Thr	Pro	Tyr	Arg	His	Gly	Asp	Ser	Val	Thr	Phe	
			85					90					95			
Ala	Cys	Lys	Thr	Asn	Phe	Ser	Met	Asn	Gly	Asn	Lys	Ser	Val	Trp	Cys	
			100					105					110			
Gln	Ala	Asn	Asn	Met	Trp	Gly	Pro	Thr	Arg	Leu	Pro	Thr	Cys	Val	Ser	
			115					120					125			
Val	Phe	Pro	Leu	Glu	Cys	Pro	Ala	Leu	Pro	Met	Ile	His	Asn	Gly	His	
			130					135					140			
His	Thr	Ser	Glu	Asn	Val	Gly	Ser	Ile	Ala	Pro	Gly	Leu	Ser	Val	Thr	
			145					150					155			160
Tyr	Ser	Cys	Glu	Ser	Gly	Tyr	Leu	Leu	Val	Gly	Glu	Lys	Ile	Ile	Asn	
			165					170					175			
Cys	Leu	Ser	Ser	Gly	Lys	Trp	Ser	Ala	Val	Pro	Pro	Thr	Cys	Glu	Glu	
			180					185					190			
Ala	Arg	Cys	Lys	Ser	Leu	Gly	Arg	Phe	Pro	Asn	Gly	Lys	Val	Lys	Glu	
			195					200					205			
Pro	Pro	Ile	Leu	Arg	Val	Gly	Val	Thr	Ala	Asn	Phe	Phe	Cys	Asp	Glu	
			210					215					220			
Gly	Tyr	Arg	Leu	Gln	Gly	Pro	Pro	Ser	Ser	Arg	Cys	Val	Ile	Ala	Gly	
			225					230					235			240
Gln	Gly	Val	Ala	Trp	Thr	Lys	Met	Pro	Val	Cys	Ser	Gly	Gly	Gly	Gly	
			245					250					255			
Ser	Leu	Gln	Cys	Tyr	Asn	Cys	Pro	Asn	Pro	Thr	Ala	Asp	Cys	Lys	Thr	
			260					265					270			
Ala	Val	Asn	Cys	Ser	Ser	Asp	Phe	Asp	Ala	Cys	Leu	Ile	Thr	Lys	Ala	
			275					280					285			
Gly	Leu	Gln	Val	Tyr	Asn	Lys	Cys	Trp	Lys	Phe	Glu	His	Cys	Asn	Phe	
			290					295					300			
Asn	Asp	Val	Thr	Thr	Arg	Leu	Arg	Glu	Asn	Glu	Leu	Thr	Tyr	Tyr	Cys	
			305					310					315			320
Cys	Lys	Lys	Asp	Leu	Cys	Asn	Phe	Asn	Glu	Gln	Leu	Glu	Asn			
			325					330								

<210> 9
<211> 1554
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 9

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tttcccgagg	atactgtaat	aacgtacaaa	tgtgaagaaa	gcttttgtaaa	aattcctggc	120
gagaaggact	cagtgtatcg	ccttaaggcc	agtcaatgg	cagatattga	agagttctgc	180
aatcgttagct	gcgagggtgcc	aacaaggcta	aattctgc	ccctcaaaca	gccttatata	240
actcagaatt	atttccagt	cggtaactgtt	gtggaaatatg	agtgccgtcc	agtttacaga	300
agagaacctt	ctctatcacc	aaaactaact	tgccttcaga	attnaaaatg	gtccacagca	360

gtcgaatttt gtaaaaagaa atcatgcctt aatccgggag aaatacggaa tggtcagatt 420
 gatgtaccag gtggcatatt atttggtgca accatctctt tctcatgtaa cacagggtac 480
 aaattatttg gctcgacttc tagttttgt cttatccat gcagctctgt ccagtggagt 540
 gaccgttgc cagagtgcag agaaaattat tgcctcggcac caccacaat tgacaatgg 600
 ataattcaag gggAACGTGA ccattatgg tataAGACGT ctgtAACGTA tgcATGTAAT 660
 aaaggattca ccatgattgg agagcactt atttattgtt ctgtGAATAA tgatGAAGGA 720
 gagtggagtg gcccaccacc tgaatgcaga tcctctggtg gcgggtggc gggcggaggt 780
 gggTCGGGTG GCGGCGGATC CATTCTGTG ggctctccct cgcctatcct aaatggccgg 840
 attagttattt attctacccc cattgctgtt ggtaccgtga taaggtacag ttgttcaggt 900
 accttccgccc tcattggaga aaaaagtcta ttatgcataa ctaaagacaa agtgatgg 960
 acctggata aacctgctcc taaaatgttattcaata aatattcttc ttgccctgag 1020
 cccatagtagc caggaggata caaaaattaga ggctctacac cctacagaca tggtgattct 1080
 gtgacatTTG CCTGTAACAC CAACTTCTCC ATGAACGGAA ACAAGTCTGT TTGGGTGCAA 1140
 gcaaaaataa tggggggcc gacacgacta ccaacctgtg taagtgttt ccctctcgag 1200
 tgtccagcac ttccatgtat ccacaatgg catcacacaa gtgagaatgt tggctccatt 1260
 gctccagatgt tgctgtgac ttacagctgt gaatctgggt acttgctgt tggagaaaaag 1320
 atcattaact gtttgttcc gggaaaatgg agtgctgtcc cccccacatg tgaagaggca 1380
 cgctgttaat ctctaggacg atttccaaat gggaaaggtaa aggagccccc aatttccgg 1440
 gttgggttaa ctgcaaactt ttctgtgtt gaagggtatc gactgcaagg cccacccct 1500
 agtcgggtgtg taattgctgg acagggagtt gcttggacca aaatgccagt atgt 1554

<210> 10

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<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =

synthetic construct

<400> 10

Asp	Cys	Gly	Leu	Pro	Pro	Asp	Val	Pro	Asn	Ala	Gln	Pro	Ala	Leu	Glu
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Gly	Arg	Thr	Ser	Phe	Pro	Glu	Asp	Thr	Val	Ile	Thr	Tyr	Lys	Cys	Glu
								20		25				30	
Glu	Ser	Phe	Val	Lys	Ile	Pro	Gly	Glu	Lys	Asp	Ser	Val	Ile	Cys	Leu
								35		40				45	
Lys	Gly	Ser	Gln	Trp	Ser	Asp	Ile	Glu	Glu	Phe	Cys	Asn	Arg	Ser	Cys
								50		55				60	
Glu	Val	Pro	Thr	Arg	Leu	Asn	Ser	Ala	Ser	Leu	Lys	Gln	Pro	Tyr	Ile
								65		70				80	
Thr	Gln	Asn	Tyr	Phe	Pro	Val	Gly	Thr	Val	Val	Glu	Tyr	Glu	Cys	Arg
								85		90				95	
Pro	Gly	Tyr	Arg	Arg	Glu	Pro	Ser	Leu	Ser	Pro	Lys	Leu	Thr	Cys	Leu
								100		105				110	
Gln	Asn	Leu	Lys	Trp	Ser	Thr	Ala	Val	Glu	Phe	Cys	Lys	Lys	Lys	Ser
								115		120				125	
Cys	Pro	Asn	Pro	Gly	Glu	Ile	Arg	Asn	Gly	Gln	Ile	Asp	Val	Pro	Gly
								130		135				140	
Gly	Ile	Leu	Phe	Gly	Ala	Thr	Ile	Ser	Phe	Ser	Cys	Asn	Thr	Gly	Tyr
								145		150				160	
Lys	Leu	Phe	Gly	Ser	Thr	Ser	Ser	Phe	Cys	Leu	Ile	Ser	Gly	Ser	Ser
								165		170				175	
Val	Gln	Trp	Ser	Asp	Pro	Leu	Pro	Glu	Cys	Arg	Glu	Ile	Tyr	Cys	Pro
								180		185				190	
Ala	Pro	Pro	Gln	Ile	Asp	Asn	Gly	Ile	Ile	Gln	Gly	Glu	Arg	Asp	His
								195		200				205	
Tyr	Gly	Tyr	Arg	Gln	Ser	Val	Thr	Tyr	Ala	Cys	Asn	Lys	Gly	Phe	Thr
								210		215				220	
Met	Ile	Gly	Glu	His	Ser	Ile	Tyr	Cys	Thr	Val	Asn	Asn	Asp	Glu	Gly

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<210> 11
<211> 990
<212> DNA
<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence:/note =
synthetic construct

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aagtttgagc attgcaattt caacgacgtc aacaaccgct tgagggaaaa tgagctaacg 180
tactactgct gcaagaagga cctgtgtaaac tttaacgaac agcttggaaa ttcctctgg 240
ggcggtggct ccggcgagg tgggtccggt ggccggcgat ccatttcttg tggctctcc 300
ccgcctatcc taaaatggccg gattagttat tattctaccc ccattgtgtg tggtaccgtg 360
ataaggta a gttgttcagg taccttcgc ctcattggag aaaaaagtct attatgcata 420
actaaagaca a aagtggatgg aacctggat aaacctgctc ctaaatgtga atatttcaat 480
aaatattctt ctgcctctga gccccatagta ccaggaggat aaaaaattag aggctctaca 540
ccctacagac atggtattc tgtgacattt gcctgtaaaa ccaacttctc catgaacgga 600
aacaagtctg ttttgttca agcaaataat atgtgggggc cgacacgact accaacctgt 660
gtaaagtgttt tccctctcga gtgtccagca cttccatgta tccacaatgg acatcacaca 720
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agtgagaatg ttggctccat tgctccagga ttgtctgtga cttacagctg tgaatctgg 780
taccttgcctg ttggagaaaa gatcattaaac tggttgcctt cgggaaaatg gagtgctgtc 840
ccccccacat gtgaagaggc acgctgtaaa tctctaggac gatttcccaa tgggaaggta 900
aaggagcctc caattctccg gggtgggtga actgcaaaact ttttctgtga tgaagggtat 960
cgactgcaag gcccacccctc tagtcggtgt 990

<210> 12
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 12
Leu Gln Cys Tyr Asn Cys Pro Asn Pro Thr Ala Asp Cys Lys Thr Ala
1 5 10 15
Val Asn Cys Ser Ser Asp Phe Asp Ala Cys Leu Ile Thr Lys Ala Gly
20 25 30
Leu Gln Val Tyr Asn Lys Cys Trp Lys Phe Glu His Cys Asn Phe Asn
35 40 45
Asp Val Thr Thr Arg Leu Arg Glu Asn Glu Leu Thr Tyr Tyr Cys Cys
50 55 60
Lys Lys Asp Leu Cys Asn Phe Asn Glu Gln Leu Glu Asn Ser Ser Gly
65 70 75 80
Gly Gly Gly Ser Gly Gly Ser Gly Gly Gly Ser Ile Ser
85 90 95
Cys Gly Ser Pro Pro Pro Ile Leu Asn Gly Arg Ile Ser Tyr Tyr Ser
100 105 110
Thr Pro Ile Ala Val Gly Thr Val Ile Arg Tyr Ser Cys Ser Gly Thr
115 120 125
Phe Arg Leu Ile Gly Glu Lys Ser Leu Leu Cys Ile Thr Lys Asp Lys
130 135 140
Val Asp Gly Thr Trp Asp Lys Pro Ala Pro Lys Cys Glu Tyr Phe Asn
145 150 155 160
Lys Tyr Ser Ser Cys Pro Glu Pro Ile Val Pro Gly Gly Tyr Lys Ile
165 170 175
Arg Gly Ser Thr Pro Tyr Arg His Gly Asp Ser Val Thr Phe Ala Cys
180 185 190
Lys Thr Asn Phe Ser Met Asn Gly Asn Lys Ser Val Trp Cys Gln Ala
195 200 205
Asn Asn Met Trp Gly Pro Thr Arg Leu Pro Thr Cys Val Ser Val Phe
210 215 220
Pro Leu Glu Cys Pro Ala Leu Pro Met Ile His Asn Gly His His Thr
225 230 235 240
Ser Glu Asn Val Gly Ser Ile Ala Pro Gly Leu Ser Val Thr Tyr Ser
245 250 255
Cys Glu Ser Gly Tyr Leu Leu Val Gly Glu Lys Ile Ile Asn Cys Leu
260 265 270
Ser Ser Gly Lys Trp Ser Ala Val Pro Pro Thr Cys Glu Glu Ala Arg
275 280 285
Cys Lys Ser Leu Gly Arg Phe Pro Asn Gly Lys Val Lys Glu Pro Pro
290 295 300
Ile Leu Arg Val Gly Val Thr Ala Asn Phe Phe Cys Asp Glu Gly Tyr
305 310 315 320
Arg Leu Gln Gly Pro Pro Ser Ser Arg Cys
325 330

<210> 13

<211> 5994
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 13
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tttctatca tctgcctaaa aaactcagtc tggactggtg ctaaggacag gtgcagacgt 180
aaatcatgtc gtaatcctcc agatcctgt aatggcatgg tgcattgtat caaaggcatc 240
cagttcgat cccaaattaa atattctgt actaaaggat accgactcat tggtcctcg 300
tctgccacat gcatcatctc aggtgatact gtcatttggg ataatgaaac acctattgt 360
gacagaattc cttgtggct accccccacc atcacaatg gagatttcat tagcaccaac 420
agagagaatt ttcactatgg atcagtggc acctaccgct gcaatcctgg aagcggaggg 480
agaaagggtt ttgagtttgggatggcc tccatataact gcaccagcaa tgacgatcaa 540
gtgggcatct ggagcggccc cgccccctc tgcattatac ctaacaaaatg cacgcctcca 600
aatgtggaaa atgaaatatt ggtatctgac aacagaagct tattttcctt aaatgaagtt 660
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 aataatgcac atgaaaaccc taaagaagtg gctatccatt tacattctca aggaggcagc 5940
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<210> 14
 <211> 2048
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 14

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 Val Gly Pro Pro Ala Pro Gly Leu Pro Phe Cys Cys Gly Gly Ser Leu
 20 25 30
 Leu Ala Val Val Val Leu Leu Ala Leu Pro Val Ala Trp Gly Gln Cys
 35 40 45
 Asn Ala Gln Cys Asn Ala Pro Glu Trp Leu Pro Phe Ala Arg Pro Thr
 50 55 60
 Asn Leu Thr Asp Glu Phe Glu Phe Pro Ile Gly Thr Tyr Leu Asn Tyr
 65 70 75 80
 Glu Cys Arg Pro Gly Tyr Ser Gly Arg Pro Phe Ser Ile Ile Cys Leu
 85 90 95
 Lys Asn Ser Val Trp Thr Gly Ala Lys Asp Arg Cys Arg Arg Lys Ser
 100 105 110
 Cys Arg Asn Pro Pro Asp Pro Val Asn Gly Met Val His Val Ile Lys
 115 120 125
 Gly Ile Gln Phe Gly Ser Gln Ile Lys Tyr Ser Cys Thr Lys Gly Tyr
 130 135 140
 Arg Leu Ile Gly Ser Ser Ala Thr Cys Ile Ile Ser Gly Asp Thr
 145 150 155 160
 Val Ile Trp Asp Asn Glu Thr Pro Ile Cys Asp Arg Ile Pro Cys Gly
 165 170 175
 Leu Pro Pro Thr Ile Thr Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu
 180 185 190
 Asn Phe His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly Ser
 195 200 205
 Gly Gly Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys
 210 215 220
 Thr Ser Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln
 225 230 235 240
 Cys Ile Ile Pro Asn Lys Cys Thr Pro Pro Asn Val Glu Asn Gly Ile
 245 250 255
 Leu Val Ser Asp Asn Arg Ser Leu Phe Ser Leu Asn Glu Val Val Glu
 260 265 270
 Phe Arg Cys Gln Pro Gly Phe Val Met Lys Gly Pro Arg Arg Val Lys
 275 280 285
 Cys Gln Ala Leu Asn Lys Trp Glu Pro Glu Leu Pro Ser Cys Ser Arg
 290 295 300
 Val Cys Gln Pro Pro Asp Val Leu His Ala Glu Arg Thr Gln Arg
 305 310 315 320
 Asp Lys Asp Asn Phe Ser Pro Gly Gln Glu Val Phe Tyr Ser Cys Glu
 325 330 335
 Pro Gly Tyr Asp Leu Arg Gly Ala Ala Ser Met Arg Cys Thr Pro Gln
 340 345 350
 Gly Asp Trp Ser Pro Ala Ala Pro Thr Cys Glu Val Lys Ser Cys Asp
 355 360 365
 Asp Phe Met Gly Gln Leu Leu Asn Gly Arg Val Leu Phe Pro Val Asn
 370 375 380
 Leu Gln Leu Gly Ala Lys Val Asp Phe Val Cys Asp Glu Gly Phe Gln
 385 390 395 400
 Leu Lys Gly Ser Ser Ala Ser Tyr Cys Val Leu Ala Gly Met Glu Ser
 405 410 415
 Leu Trp Asn Ser Ser Val Pro Val Cys Glu Gln Ile Phe Cys Pro Ser
 420 425 430
 Pro Pro Val Ile Pro Asn Gly Arg His Thr Gly Lys Pro Leu Glu Val
 435 440 445
 Phe Pro Phe Gly Lys Ala Val Asn Tyr Thr Cys Asp Pro His Pro Asp
 450 455 460
 Arg Gly Thr Ser Phe Asp Leu Ile Gly Glu Ser Thr Ile Arg Cys Thr
 465 470 475 480
 Ser Asp Pro Gln Gly Asn Gly Val Trp Ser Ser Pro Ala Pro Arg Cys

485	490	495
Gly Ile Leu Gly His Cys Gln Ala Pro Asp His Phe Leu Phe Ala Lys		
500	505	510
Leu Lys Thr Gln Thr Asn Ala Ser Asp Phe Pro Ile Gly Thr Ser Leu		
515	520	525
Lys Tyr Glu Cys Arg Pro Glu Tyr Tyr Gly Arg Pro Phe Ser Ile Thr		
530	535	540
Cys Leu Asp Asn Leu Val Trp Ser Ser Pro Lys Asp Val Cys Lys Arg		
545	550	555
Lys Ser Cys Lys Thr Pro Pro Asp Pro Val Asn Gly Met Val His Val		
565	570	575
Ile Thr Asp Ile Gln Val Gly Ser Arg Ile Asn Tyr Ser Cys Thr Thr		
580	585	590
Gly His Arg Leu Ile Gly His Ser Ser Ala Glu Cys Ile Leu Ser Gly		
595	600	605
Asn Ala Ala His Trp Ser Thr Lys Pro Pro Ile Cys Gln Arg Ile Pro		
610	615	620
Cys Gly Leu Pro Pro Thr Ile Ala Asn Gly Asp Phe Ile Ser Thr Asn		
625	630	635
Arg Glu Asn Phe His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro		
645	650	655
Gly Ser Gly Gly Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile		
660	665	670
Tyr Cys Thr Ser Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala		
675	680	685
Pro Gln Cys Ile Ile Pro Asn Lys Cys Thr Pro Pro Asn Val Glu Asn		
690	695	700
Gly Ile Leu Val Ser Asp Asn Arg Ser Leu Phe Ser Leu Asn Glu Val		
705	710	715
Val Glu Phe Arg Cys Gln Pro Gly Phe Val Met Lys Gly Pro Arg Arg		
725	730	735
Val Lys Cys Gln Ala Leu Asn Lys Trp Glu Pro Glu Leu Pro Ser Cys		
740	745	750
Ser Arg Val Cys Gln Pro Pro Asp Val Leu His Ala Glu Arg Thr		
755	760	765
Gln Arg Asp Lys Asp Asn Phe Ser Pro Gly Gln Glu Val Phe Tyr Ser		
770	775	780
Cys Glu Pro Gly Tyr Asp Leu Arg Gly Ala Ala Ser Met Arg Cys Thr		
785	790	795
800		
Pro Gln Gly Asp Trp Ser Pro Ala Ala Pro Thr Cys Glu Val Lys Ser		
805	810	815
Cys Asp Asp Phe Met Gly Gln Leu Leu Asn Gly Arg Val Leu Phe Pro		
820	825	830
Val Asn Leu Gln Leu Gly Ala Lys Val Asp Phe Val Cys Asp Glu Gly		
835	840	845
Phe Gln Leu Lys Gly Ser Ser Ala Ser Tyr Cys Val Leu Ala Gly Met		
850	855	860
Glu Ser Leu Trp Asn Ser Ser Val Pro Val Cys Glu Gln Ile Phe Cys		
865	870	875
880		
Pro Ser Pro Pro Val Ile Pro Asn Gly Arg His Thr Gly Lys Pro Leu		
885	890	895
Glu Val Phe Pro Phe Gly Lys Ala Val Asn Tyr Thr Cys Asp Pro His		
900	905	910
910		
Pro Asp Arg Gly Thr Ser Phe Asp Leu Ile Gly Glu Ser Thr Ile Arg		
915	920	925
Cys Thr Ser Asp Pro Gln Gly Asn Gly Val Trp Ser Ser Pro Ala Pro		
930	935	940
Arg Cys Gly Ile Leu Gly His Cys Gln Ala Pro Asp His Phe Leu Phe		
945	950	955
960		
Ala Lys Leu Lys Thr Gln Thr Asn Ala Ser Asp Phe Pro Ile Gly Thr		
965	970	975

Ser Leu Lys Tyr Glu Cys Arg Pro Glu Tyr Tyr Gly Arg Pro Phe Ser
 980 985 990
 Ile Thr Cys Leu Asp Asn Leu Val Trp Ser Ser Pro Lys Asp Val Cys
 995 1000 1005
 Lys Arg Lys Ser Cys Lys Thr Pro Pro Asp Pro Val Asn Gly Met Val
 1010 1015 1020
 His Val Ile Thr Asp Ile Gln Val Gly Ser Arg Ile Asn Tyr Ser Cys
 1025 1030 1035 1040
 Thr Thr Gly His Arg Leu Ile Gly His Ser Ser Ala Glu Cys Ile Leu
 1045 1050 1055
 Ser Gly Asn Thr Ala His Trp Ser Thr Lys Pro Pro Ile Cys Gln Arg
 1060 1065 1070
 Ile Pro Cys Gly Leu Pro Pro Thr Ile Ala Asn Gly Asp Phe Ile Ser
 1075 1080 1085
 Thr Asn Arg Glu Asn Phe His Tyr Gly Ser Val Val Thr Tyr Arg Cys
 1090 1095 1100
 Asn Leu Gly Ser Arg Gly Arg Lys Val Phe Glu Leu Val Gly Glu Pro
 1105 1110 1115 1120
 Ser Ile Tyr Cys Thr Ser Asn Asp Asp Gln Val Gly Ile Trp Ser Gly
 1125 1130 1135
 Pro Ala Pro Gln Cys Ile Ile Pro Asn Lys Cys Thr Pro Pro Asn Val
 1140 1145 1150
 Glu Asn Gly Ile Leu Val Ser Asp Asn Arg Ser Leu Phe Ser Leu Asn
 1155 1160 1165
 Glu Val Val Glu Phe Arg Cys Gln Pro Gly Phe Val Met Lys Gly Pro
 1170 1175 1180
 Arg Arg Val Lys Cys Gln Ala Leu Asn Lys Trp Glu Pro Glu Leu Pro
 1185 1190 1195 1200
 Ser Cys Ser Arg Val Cys Gln Pro Pro Pro Glu Ile Leu His Gly Glu
 1205 1210 1215
 His Thr Pro Ser His Gln Asp Asn Phe Ser Pro Gly Gln Glu Val Phe
 1220 1225 1230
 Tyr Ser Cys Glu Pro Gly Tyr Asp Leu Arg Gly Ala Ala Ser Leu His
 1235 1240 1245
 Cys Thr Pro Gln Gly Asp Trp Ser Pro Glu Ala Pro Arg Cys Ala Val
 1250 1255 1260
 Lys Ser Cys Asp Asp Phe Leu Gly Gln Leu Pro His Gly Arg Val Leu
 1265 1270 1275 1280
 Phe Pro Leu Asn Leu Gln Leu Gly Ala Lys Val Ser Phe Val Cys Asp
 1285 1290 1295
 Glu Gly Phe Arg Leu Lys Gly Ser Ser Val Ser His Cys Val Leu Val
 1300 1305 1310
 Gly Met Arg Ser Leu Trp Asn Asn Ser Val Pro Val Cys Glu His Ile
 1315 1320 1325
 Phe Cys Pro Asn Pro Pro Ala Ile Leu Asn Gly Arg His Thr Gly Thr
 1330 1335 1340
 Pro Ser Gly Asp Ile Pro Tyr Gly Lys Glu Ile Ser Tyr Thr Cys Asp
 1345 1350 1355 1360
 Pro His Pro Asp Arg Gly Met Thr Phe Asn Leu Ile Gly Glu Ser Thr
 1365 1370 1375
 Ile Arg Cys Thr Ser Asp Pro His Gly Asn Gly Val Trp Ser Ser Pro
 1380 1385 1390
 Ala Pro Arg Cys Glu Leu Ser Val Arg Ala Gly His Cys Lys Thr Pro
 1395 1400 1405
 Glu Gln Phe Pro Phe Ala Ser Pro Thr Ile Pro Ile Asn Asp Phe Glu
 1410 1415 1420
 Phe Pro Val Gly Thr Ser Leu Asn Tyr Glu Cys Arg Pro Gly Tyr Phe
 1425 1430 1435 1440
 Gly Lys Met Phe Ser Ile Ser Cys Leu Glu Asn Leu Val Trp Ser Ser
 1445 1450 1455
 Val Glu Asp Asn Cys Arg Arg Lys Ser Cys Gly Pro Pro Glu Pro

1460	1465	1470
Phe Asn Gly Met Val His Ile Asn Thr Asp Thr Gln Phe	Gly Ser Thr	
1475	1480	1485
Val Asn Tyr Ser Cys Asn Glu Gly Phe Arg Leu Ile	Gly Ser Pro Ser	
1490	1495	1500
Thr Thr Cys Leu Val Ser Gly Asn Asn Val Thr Trp Asp	Lys Lys Ala	
1505	1510	1515
Pro Ile Cys Glu Ile Ile Ser Cys Glu Pro Pro Pro Thr	Ile Ser Asn	
1525	1530	1535
Gly Asp Phe Tyr Ser Asn Asn Arg Thr Ser Phe His Asn	Gly Thr Val	
1540	1545	1550
Val Thr Tyr Gln Cys His Thr Gly Pro Asp Gly Glu Gln	Leu Phe Glu	
1555	1560	1565
Leu Val Gly Glu Arg Ser Ile Tyr Cys Thr Ser Lys Asp	Asp Gln Val	
1570	1575	1580
Gly Val Trp Ser Ser Pro Pro Pro Arg Cys Ile Ser Thr	Asn Lys Cys	
1585	1590	1595
Thr Ala Pro Glu Val Glu Asn Ala Ile Arg Val Pro	Gly Asn Arg Ser	
1605	1610	1615
Phe Phe Ser Leu Thr Glu Ile Ile Arg Phe Arg Cys Gln	Pro Gly Phe	
1620	1625	1630
Val Met Val Gly Ser His Thr Val Gln Cys Gln Thr Asn	Gly Arg Trp	
1635	1640	1645
Gly Pro Lys Leu Pro His Cys Ser Arg Val Cys Gln	Pro Pro Pro Glu	
1650	1655	1660
Ile Leu His Gly Glu His Thr Leu Ser His Gln Asp Asn	Phe Ser Pro	
1665	1670	1675
Gly Gln Glu Val Phe Tyr Ser Cys Glu Pro Ser Tyr Asp	Leu Arg Gly	
1685	1690	1695
Ala Ala Ser Leu His Cys Thr Pro Gln Gly Asp Trp Ser	Pro Glu Ala	
1700	1705	1710
Pro Arg Cys Thr Val Lys Ser Cys Asp Asp Phe Leu	Gly Gln Leu Pro	
1715	1720	1725
His Gly Arg Val Leu Leu Pro Leu Asn Leu Gln Leu	Gly Ala Lys Val	
1730	1735	1740
Ser Phe Val Cys Asp Glu Gly Phe Arg Leu Lys Gly Arg	Ser Ala Ser	
1745	1750	1755
His Cys Val Leu Ala Gly Met Lys Ala Leu Trp Asn Ser	Ser Val Pro	
1765	1770	1775
Val Cys Glu Gln Ile Phe Cys Pro Asn Pro Pro Ala Ile	Leu Asn Gly	
1780	1785	1790
Arg His Thr Gly Thr Pro Phe Gly Asp Ile Pro Tyr	Gly Lys Glu Ile	
1795	1800	1805
Ser Tyr Ala Cys Asp Thr His Pro Asp Arg Gly Met	Thr Phe Asn Leu	
1810	1815	1820
Ile Gly Glu Ser Ser Ile Arg Cys Thr Ser Asp Pro	Gln Gly Asn Gly	
1825	1830	1835
Val Trp Ser Ser Pro Ala Pro Arg Cys Glu Leu Ser Val	Pro Ala Ala	
1845	1850	1855
Cys Pro His Pro Pro Lys Ile Gln Asn Gly His Tyr	Ile Gly Gly His	
1860	1865	1870
Val Ser Leu Tyr Leu Pro Gly Met Thr Ile Ser Tyr	Thr Cys Asp Pro	
1875	1880	1885
Gly Tyr Leu Leu Val Gly Lys Gly Phe Ile Phe Cys	Thr Asp Gln Gly	
1890	1895	1900
Ile Trp Ser Gln Leu Asp His Tyr Cys Lys Glu Val Asn	Cys Ser Phe	
1905	1910	1915
Pro Leu Phe Met Asn Gly Ile Ser Lys Glu Leu Glu Met	Lys Lys Val	
1925	1930	1935
Tyr His Tyr Gly Asp Tyr Val Thr Leu Lys Cys Glu Asp	Gly Tyr Thr	

1940	1945	1950
Leu	Glu	Gly
Ser	Pro	Trp
Pro	Trp	Ser
Gln	Cys	Gln
Ala	Asp	Asp
Arg	Trp	Asp
1955	1960	1965
Pro	Pro	Leu
Leu	Ala	Lys
Cys	Thr	Ser
Thr	Ser	Arg
Ala	His	Asp
His	Asp	Ala
Leu	Ile	Val
1970	1975	1980
Gly	Thr	Leu
Leu	Ser	Gly
Gly	Thr	Ile
Ile	Phe	Phe
Phe	Ile	Leu
Leu	Ile	Ile
Ile	Phe	Leu
1985	1990	1995
Ser	Trp	Ile
Ile	Leu	Lys
Lys	His	Arg
Arg	Lys	Gly
Gly	Asn	Asn
Asn	Ala	His
His	Glu	Asn
Pro	Lys	Glu
Glu	Val	Val
Val	Ala	Ile
Ile	His	His
His	Ser	Gln
Gly	Gly	Gly
Gly	Ser	Ser
Ser	Val	Val
2005	2010	2015
Pro	Lys	Glu
Glu	Val	Ala
Val	Ile	His
Ile	His	Leu
His	Ser	Gln
Gly	Gly	Gly
Gly	Ser	Ser
Ser	Val	Val
2020	2025	2030
His	Pro	Arg
Pro	Arg	Thr
Arg	Thr	Leu
Thr	Leu	Gln
Gln	Thr	Asn
Asn	Glu	Glu
Glu	Asn	Ser
Asn	Ser	Arg
Arg	Val	Val
Val	Leu	Pro
2035	2040	2045

<210> 15
<211> 1029
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 15
tgtgaggagc caccaacatt tgaagctatg gagctcattt gtaaacaaaa accctactat 60
gagattgggt aacgagtaga ttataagtgt aaaaaaggat acttcttat acctcccttt 120
gccaccata ctatgttgc tcggaatcat acatggctac ctgtctcaga tgacgcctgt 180
tatagagaaa catgtccata tatacggat cctttaatg gccaaggcagt ccctgcaaat 240
gggacttacg agttgggtt tcagatgcac tttattttgtt atgaggggtt ttacttaatt 300
ggtgaagaaa ttctatattt tgaacttaaa ggatcgatgtt caatttggag cggttaagcccc 360
ccaatatgtt aaaaagggtttt gtgtacacca cctccaaaaaa taaaaaatgg aaaacacacc 420
tttagtgaag tagaagtatt tgagtatctt gatgcgtt cttatagtttg tgatcctgca 480
cctggaccag atccattttt acttattttttt gagagcacga tttatttttttgg tgacaattca 540
gtgtggagtc gtgtgttcc agagtgtttt gtggtcaat gtcgattttcc agtagtcgaa 600
aatggaaaac agatatcagg atttggaaaa aaattttact acaaagcaac agttatgtttt 660
gaatgcata agggttttt cctcgatggc agcgacacaa ttgtctgtt cagtaacagt 720
acttgggatc cccaggattcc aaagtgttcc aaagtgtcga cttcttccac tacaaaatct 780
ccagcgttcca gtgcctcagg tccttaggcct acttacaagc ctccagttcc aaattatccca 840
ggatatccta aacctgagga aggaataactt gacagttttgg atgtttgggtt cattgctgtg 900
attgttatttgc ccatagttgtt tggagtttgc gtaattttgtt ttgtccctt cagatatctt 960
caaaggagga agaagaaagg cacataccta actgtatgaga cccacagaga agtaaaaattt 1020
acttctctc 1029

<210> 16
<211> 378
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 16
Met Glu Pro Pro Gly Arg Arg Glu Cys Pro Phe Pro Ser Trp Arg Phe
1 5 10 15
Phe Pro Gly Leu Leu Leu Ala Ala Met Val Leu Leu Leu Tyr Ser Phe
20 25 30
Ser Asp Ala Cys Glu Glu Pro Pro Thr Phe Glu Ala Met Glu Leu Ile
35 40 45
Gly Lys Pro Lys Pro Tyr Tyr Glu Ile Gly Glu Arg Val Asp Tyr Lys

50	55	60
Cys Lys Lys Gly Tyr Phe Tyr Ile Pro Pro Leu Ala Thr His Thr Ile		
65	70	75
Cys Asp Arg Asn His Thr Trp Leu Pro Val Ser Asp Asp Ala Cys Tyr		80
85	90	95
Arg Glu Thr Cys Pro Tyr Ile Arg Asp Pro Leu Asn Gly Gln Ala Val		
100	105	110
Pro Ala Asn Gly Thr Tyr Glu Phe Gly Tyr Gln Met His Phe Ile Cys		
115	120	125
Asn Glu Gly Tyr Tyr Leu Ile Gly Glu Glu Ile Leu Tyr Cys Glu Leu		
130	135	140
Lys Gly Ser Val Ala Ile Trp Ser Gly Lys Pro Pro Ile Cys Glu Lys		
145	150	155
Val Leu Cys Thr Pro Pro Lys Ile Lys Asn Gly Lys His Thr Phe		160
165	170	175
Ser Glu Val Glu Val Phe Glu Tyr Leu Asp Ala Val Thr Tyr Ser Cys		
180	185	190
Asp Pro Ala Pro Gly Pro Asp Pro Phe Ser Leu Ile Gly Glu Ser Thr		
195	200	205
Ile Tyr Cys Gly Asp Asn Ser Val Trp Ser Arg Ala Ala Pro Glu Cys		
210	215	220
Lys Val Val Lys Cys Arg Phe Pro Val Val Glu Asn Gly Lys Gln Ile		
225	230	235
Ser Gly Phe Gly Lys Phe Tyr Tyr Lys Ala Thr Val Met Phe Glu		240
245	250	255
Cys Asp Lys Gly Phe Tyr Leu Asp Gly Ser Asp Thr Ile Val Cys Asp		
260	265	270
Ser Asn Ser Thr Trp Asp Pro Pro Val Pro Lys Cys Leu Lys Val Ser		
275	280	285
Thr Ser Ser Thr Thr Lys Ser Pro Ala Ser Ser Ala Ser Gly Pro Arg		
290	295	300
Pro Thr Tyr Lys Pro Pro Val Ser Asn Tyr Pro Gly Tyr Pro Lys Pro		
305	310	315
Glu Glu Gly Ile Leu Asp Ser Leu Asp Val Trp Val Ile Ala Val Ile		320
325	330	335
Val Ile Ala Ile Val Val Gly Val Ala Val Ile Cys Val Val Pro Tyr		
340	345	350
Arg Tyr Leu Gln Arg Arg Lys Lys Lys Gly Thr Tyr Leu Thr Asp Glu		
355	360	365
Thr His Arg Glu Val Lys Phe Thr Ser Leu		
370	375	

<210> 17
<211> 440
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 17		
Met Glu Val Ser Ser Arg Ser Ser Glu Pro Leu Asp Pro Val Trp Leu		
1	5	10
Leu Val Ala Phe Gly Arg Gly Gly Val Lys Leu Glu Val Leu Leu Leu		15
20	25	30
Phe Leu Leu Pro Phe Thr Leu Gly His Cys Pro Ala Pro Ser Gln Leu		
35	40	45
Pro Ser Ala Lys Pro Ile Asn Leu Thr Asp Glu Ser Met Phe Pro Ile		
50	55	60

Gly Thr Tyr Leu Leu Tyr Glu Cys Leu Pro Gly Tyr Ile Lys Arg Gln
 65 70 75 80
 Phe Ser Ile Thr Cys Lys Gln Asp Ser Thr Trp Thr Ser Ala Glu Asp
 85 90 95
 Lys Cys Ile Arg Lys Gln Cys Lys Thr Pro Ser Asp Pro Glu Asn Gly
 100 105 110
 Leu Val His Val His Thr Gly Ile Gln Phe Gly Ser Arg Ile Asn Tyr
 115 120 125
 Thr Cys Asn Gln Gly Tyr Arg Leu Ile Gly Ser Ser Ala Val Cys
 130 135 140
 Val Ile Thr Asp Gln Ser Val Asp Trp Asp Thr Glu Ala Pro Ile Cys
 145 150 155 160
 Glu Trp Ile Pro Cys Glu Ile Pro Pro Gly Ile Pro Asn Gly Asp Phe
 165 170 175
 Phe Ser Ser Thr Arg Glu Asp Phe His Tyr Gly Met Val Val Thr Tyr
 180 185 190
 Arg Cys Asn Thr Asp Ala Arg Gly Lys Ala Leu Phe Asn Leu Val Gly
 195 200 205
 Glu Pro Ser Leu Tyr Cys Thr Ser Asn Asp Gly Glu Ile Gly Val Trp
 210 215 220
 Ser Gly Pro Pro Pro Gln Cys Ile Glu Leu Asn Lys Cys Thr Pro Pro
 225 230 235 240
 Pro Tyr Val Glu Asn Ala Val Met Leu Ser Glu Asn Arg Ser Leu Phe
 245 250 255
 Ser Leu Arg Asp Ile Val Glu Phe Arg Cys His Pro Gly Phe Ile Met
 260 265 270
 Lys Gly Ala Ser Ser Val His Cys Gln Ser Leu Asn Lys Trp Glu Pro
 275 280 285
 Glu Leu Pro Ser Cys Phe Lys Gly Val Ile Cys Arg Leu Pro Gln Glu
 290 295 300
 Met Ser Gly Phe Gln Lys Gly Leu Gly Met Lys Lys Glu Tyr Tyr Tyr
 305 310 315 320
 Gly Glu Asn Val Thr Leu Glu Cys Glu Asp Gly Tyr Thr Leu Glu Gly
 325 330 335
 Ser Ser Gln Ser Gln Cys Gln Ser Asp Gly Ser Trp Asn Pro Leu Leu
 340 345 350
 Ala Lys Cys Val Ser Arg Ser Ile Ser Gly Leu Ile Val Gly Ile Phe
 355 360 365
 Ile Gly Ile Ile Val Phe Ile Leu Val Ile Ile Val Phe Ile Trp Met
 370 375 380
 Ile Leu Lys Tyr Lys Lys Arg Asn Thr Thr Asp Glu Lys Tyr Lys Glu
 385 390 395 400
 Val Gly Ile His Leu Asn Tyr Lys Glu Asp Ser Cys Val Arg Leu Gln
 405 410 415
 Ser Leu Leu Thr Ser Gln Glu Asn Ser Ser Thr Thr Ser Pro Ala Arg
 420 425 430
 Asn Ser Leu Thr Gln Glu Val Ser
 435 440

<210> 18
 <211> 232
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 18
 Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

1	5	10	15												
Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro
		20				25						30			
Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val
		35				40						45			
Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val
		50				55					60				
Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Gln	
		65				70				75		80			
Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln
		85							90			95			
Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala
		100					105					110			
Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro
		115					120					125			
Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr
		130				135					140				
Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser
		145				150				155		160			
Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr
		165					170					175			
Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Pro	Phe	Phe	Leu	Tyr
		180					185					190			
Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe
		195				200					205				
Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys
		210				215					220				
Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys								
		225				230									

<210> 19
<211> 454.
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
synthetic construct

1	5	10	15												
Gly	Ser	Ala	Ser	Ala	Pro	Thr	Leu	Phe	Pro	Leu	Val	Ser	Cys	Glu	Asn
Ser	Pro	Ser	Asp	Thr	Ser	Ser	Val	Ala	Val	Gly	Cys	Leu	Ala	Gln	Asp
							20		25			30			
Phe	Leu	Pro	Asp	Ser	Ile	Thr	Phe	Ser	Trp	Lys	Tyr	Lys	Asn	Asn	Ser
							35		40			45			
Asp	Ile	Ser	Ser	Thr	Arg	Gly	Phe	Pro	Ser	Val	Leu	Arg	Gly	Gly	Lys
						50		55			60				
Tyr	Ala	Ala	Thr	Ser	Gln	Val	Leu	Leu	Pro	Ser	Lys	Asp	Val	Met	Gln
						65		70			75		80		
Gly	Thr	Asp	Glu	His	Val	Val	Cys	Lys	Val	Gln	His	Pro	Asn	Gly	Asn
						85		90			95				
Lys	Glu	Lys	Asn	Val	Pro	Leu	Pro	Val	Ile	Ala	Glu	Leu	Pro	Pro	Lys
						100		105			110				
Val	Ser	Val	Phe	Val	Pro	Pro	Arg	Asp	Gly	Phe	Phe	Gly	Asn	Pro	Arg
						115		120			125				
Ser	Lys	Ser	Lys	Leu	Ile	Cys	Gln	Ala	Thr	Gly	Phe	Ser	Pro	Arg	Gln
						130		135			140				
Ile	Gln	Val	Ser	Trp	Leu	Arg	Glu	Gly	Lys	Gln	Val	Gly	Ser	Gly	Val
						145		150			155		160		

Thr Thr Asp Gln Val Gln Ala Glu Ala Lys Glu Ser Gly Pro Thr Thr
 165 170 175
 Tyr Lys Val Thr Ser Thr Leu Thr Ile Lys Glu Ser Asp Trp Leu Ser
 180 185 190
 Gln Ser Met Phe Thr Cys Arg Val Asp His Arg Gly Leu Thr Phe Gln
 195 200 205
 Gln Asn Ala Ser Ser Met Cys Val Pro Asp Gln Asp Thr Ala Ile Arg
 210 215 220
 Val Phe Ala Ile Pro Pro Ser Phe Ala Ser Ile Phe Leu Thr Lys Ser
 225 230 235 240
 Thr Lys Leu Thr Cys Leu Val Thr Asp Leu Thr Thr Tyr Asp Ser Val
 245 250 255
 Thr Ile Ser Trp Thr Arg Gln Asn Gly Glu Ala Val Lys Thr His Thr
 260 265 270
 Asn Ile Ser Glu Ser His Pro Asn Ala Thr Phe Ser Ala Val Gly Glu
 275 280 285
 Ala Ser Ile Cys Glu Asp Asp Trp Asn Ser Gly Glu Arg Phe Thr Cys
 290 295 300
 Thr Val Thr His Thr Asp Leu Pro Ser Pro Leu Lys Gln Thr Ile Ser
 305 310 315 320
 Arg Pro Lys Gly Val Ala Leu His Arg Pro Asp Val Tyr Leu Leu Pro
 325 330 335
 Pro Ala Arg Glu Gln Leu Asn Leu Arg Glu Ser Ala Thr Ile Thr Cys
 340 345 350
 Leu Val Thr Gly Phe Ser Pro Ala Asp Val Phe Val Gln Trp Met Gln
 355 360 365
 Arg Gly Gln Pro Leu Ser Pro Glu Lys Tyr Val Thr Ser Ala Pro Met
 370 375 380
 Pro Glu Pro Gln Ala Pro Gly Arg Tyr Phe Ala His Ser Ile Leu Thr
 385 390 395 400
 Val Ser Glu Glu Glu Trp Asn Thr Gly Glu Thr Tyr Thr Cys Val Val
 405 410 415
 Ala His Glu Ala Leu Pro Asn Arg Val Thr Glu Arg Thr Val Asp Lys
 420 425 430
 Ser Thr Gly Lys Pro Thr Leu Tyr Asn Val Ser Leu Val Met Ser Asp
 435 440 445
 Thr Ala Gly Thr Cys Tyr
 450

<210> 20
 <211> 1530
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 20
 atgggcgccc cggcctgct cgggttttc ttggctctcg tcgcaccggg ggtcctcg 60
 atttcttgtg gcttcctcc gcctatcta aatggccgga ttagttatta ttctaccccc 120
 attgctgttg gtaccgtat aaggtacagt tgttcaggtt ccttccgcct cattggagaa 180
 aaaagtctat tatgcataac taaagacaaa gtggatggaa cctggataa acctgctcct 240
 aaatgtgaat attcaataa atattctct tgcctgagc ccatagttacc aggaggatac 300
 aaaatttagag gctctacacc ctacagacat ggtgattctg tgacatttgc ctgtaaaacc 360
 aacttctcca tgaacggaaa caagtctgtt tggtgtcaag caaataatat gtggggccg 420
 acacgactac caacctgtgt aagtgtttc cctctcgagt gtccagcact tccttatgatc 480
 cacaatggac atcacacaag tgagaatgtt ggctccattg ctccaggatt gtctgtgact 540
 tacagctgtg aatctggta cttgcttgc ggagaaaaga tcattaactg tttgtcttcg 600
 ggaaaaatgga gtgtgtcccc ccccacatgt gaagaggcac gctgtaaatc tctaggacga 660

tttcccaatg ggaaggtaaa ggagcctcca attctccggg ttggtgtaac tgcaaactt 720
 ttctgtatcg aagggtatcg actgcaaggc ccacccctca gtcgggtgt aattgctgga 780
 caggagttg cttggaccaa aatgccatgt aatggaaa tttttgcgg actgcggccg 840
 cagtcttaga acaaaaactca cacatgccc ccgtccccag cacctgaact cctgggggg 900
 ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccct 960
 gaggtcacat gcgtgggtt ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg 1020
 tacgtggacg gcgtggaggt gcataatgcc aagacaaggc cgccggagga gcagtacaac 1080
 agcacgtacc gtgtggtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag 1140
 gagtacaagt gcaaggcttc caacaaagcc ctccctgatcc ccacatcgagaa aaccatctcc 1200
 aaagccaaag ggcagccccg agaaccacag gtgtacaccc tgcccccatt ccggaggag 1260
 atgaccaaga accaggttcag cctgacctgc ctggtaaaag gcttctatcc cagcgacatc 1320
 gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctccctg 1380
 ctggactccg acggctcctt cttcccttat agcaagctca ccgtggacaa gagcaggtgg 1440
 cagcagggga acgtttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg 1500
 cagaagagcc tctccctgtc cccgggtaaa 1530

<210> 21
 <211> 510
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 21
 Met Gly Ala Ala Gly Leu Leu Gly Val Phe Leu Ala Leu Val Ala Pro
 1 5 10 15
 Gly Val Leu Gly Ile Ser Cys Gly Ser Pro Pro Pro Ile Leu Asn Gly
 20 25 30
 Arg Ile Ser Tyr Tyr Ser Thr Pro Ile Ala Val Gly Thr Val Ile Arg
 35 40 45
 Tyr Ser Cys Ser Gly Thr Phe Arg Leu Ile Gly Glu Lys Ser Leu Leu
 50 55 60
 Cys Ile Thr Lys Asp Lys Val Asp Gly Thr Trp Asp Lys Pro Ala Pro
 65 70 75 80
 Lys Cys Glu Tyr Phe Asn Lys Tyr Ser Ser Cys Pro Glu Pro Ile Val
 85 90 95
 Pro Gly Gly Tyr Lys Ile Arg Gly Ser Thr Pro Tyr Arg His Gly Asp
 100 105 110
 Ser Val Thr Phe Ala Cys Lys Thr Asn Phe Ser Met Asn Gly Asn Lys
 115 120 125
 Ser Val Trp Cys Gln Ala Asn Asn Met Trp Gly Pro Thr Arg Leu Pro
 130 135 140
 Thr Cys Val Ser Val Phe Pro Leu Glu Cys Pro Ala Leu Pro Met Ile
 145 150 155 160

 His Asn Gly His His Thr Ser Glu Asn Val Gly Ser Ile Ala Pro Gly
 165 170 175
 Leu Ser Val Thr Tyr Ser Cys Glu Ser Gly Tyr Leu Leu Val Gly Glu
 180 185 190
 Lys Ile Ile Asn Cys Leu Ser Ser Gly Lys Trp Ser Ala Val Pro Pro
 195 200 205
 Thr Cys Glu Glu Ala Arg Cys Lys Ser Leu Gly Arg Phe Pro Asn Gly
 210 215 220
 Lys Val Lys Glu Pro Pro Ile Leu Arg Val Gly Val Thr Ala Asn Phe
 225 230 235 240
 Phe Cys Asp Glu Gly Tyr Arg Leu Gln Gly Pro Pro Ser Ser Arg Cys
 245 250 255
 Val Ile Ala Gly Gln Gly Val Ala Trp Thr Lys Met Pro Val Cys Glu
 260 265 270

Glu	Ile	Phe	Cys	Pro	Leu	Arg	Pro	Gln	Ser	Arg	Asp	Lys	Thr	His	Thr
275							280					285			
Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe
290							295					300			
Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro
305							310				315				320
Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val
							325				330				335
Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr
							340				345				350
Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val
							355				360				365
Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys
							370				375				380
Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Val	Pro	Ile	Glu	Lys	Thr	Ile	Ser
385							390				395				400
Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro
							405				410				415
Ser	Arg	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val
							420				425				430
Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly
							435				440				445
Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp
							450				455				460
Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp
465							470				475				480
Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His
							485				490				495
Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys		
							500				505				510

<210> 22

<211> 233

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 22

Glu	Pro	Arg	Ile	Pro	Lys	Pro	Ser	Thr	Pro	Pro	Gly	Ser	Ser	Cys	Pro	
1					5				10					15		
Pro	Gly	Asn	Ile	Leu	Gly	Gly	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Lys	
									20			25			30	
Pro	Lys	Asp	Ala	Leu	Met	Ile	Ser	Leu	Thr	Pro	Lys	Val	Thr	Cys	Val	
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Val	Val	Asp	Val	Ser	Glu	Asp	Asp	Pro	Asp	Val	His	Val	Ser	Trp	Phe	
									50			55			60	
Val	Asp	Asn	Lys	Glu	Val	His	Thr	Ala	Trp	Thr	Gln	Pro	Arg	Glu	Ala	
								65			70			75		80
Gln	Tyr	Asn	Ser	Thr	Phe	Arg	Val	Val	Ser	Ala	Leu	Pro	Ile	Gln	His	
								85			90			95		
Gln	Asp	Trp	Met	Arg	Gly	Lys	Glu	Phe	Lys	Cys	Lys	Val	Asn	Asn	Lys	
								100			105			110		
Ala	Leu	Pro	Ala	Pro	Ile	Glu	Arg	Thr	Ile	Ser	Lys	Pro	Lys	Gly	Arg	
								115			120			125		
Ala	Gln	Thr	Pro	Gln	Val	Tyr	Thr	Ile	Pro	Pro	Pro	Arg	Glu	Gln	Met	
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Ser	Lys	Lys	Lys	Val	Ser	Leu	Thr	Cys	Leu	Val	Thr	Asn	Phe	Phe	Ser	

145	150	155	160
Glu Ala Ile Ser Val Glu Trp Glu Arg Asn Gly Glu Leu Glu Gln Asp			
165	170	175	
Tyr Lys Asn Thr Pro Pro Ile Leu Asp Ser Asp Gly Thr Tyr Phe Leu			
180	185	190	
Tyr Ser Lys Leu Thr Val Asp Thr Asp Ser Trp Leu Gln Gly Glu Ile			
195	200	205	
Phe Thr Cys Ser Val Val His Glu Ala Leu His Asn His His Thr Gln			
210	215	220	
Lys Asn Leu Ser Arg Ser Pro Gly Lys			
225	230		

<210> 23
<211> 4860
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
synthetic construct

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 aagttgttg atgactttgc tcaatgttgc tacacattga ctgagttgg ctgcctact 4860

<210> 24
 <211> 1620
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/note =
 synthetic construct

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 Asp Ile Phe Val His Asp Phe Pro Arg Lys Gln Lys Thr Leu Phe Gln
 35 40 45

Thr Arg Val Asp Met Asn Pro Ala Gly Gly Met Leu Val Thr Pro Thr
 50 55 60
 Ile Glu Ile Pro Ala Lys Glu Val Ser Thr Asp Ser Arg Gln Asn Gln
 65 70 75 80
 Tyr Val Val Val Gln Val Thr Gly Pro Gln Val Arg Leu Glu Lys Val
 85 90 95
 Val Leu Leu Ser Tyr Gln Ser Ser Phe Leu Phe Ile Gln Thr Asp Lys
 100 105 110
 Gly Ile Tyr Thr Pro Gly Ser Pro Val Leu Tyr Arg Val Phe Ser Met
 115 120 125
 Asp His Asn Thr Ser Lys Met Asn Lys Thr Val Ile Val Glu Phe Gln
 130 135 140
 Thr Pro Glu Gly Ile Leu Val Ser Ser Asn Ser Val Asp Leu Asn Phe
 145 150 155 160
 Phe Trp Pro Tyr Asn Leu Pro Asp Leu Val Ser Leu Gly Thr Trp Arg
 165 170 175
 Ile Val Ala Lys Tyr Glu His Ser Pro Glu Asn Tyr Thr Ala Tyr Phe
 180 185 190
 Asp Val Arg Lys Tyr Val Leu Pro Ser Phe Glu Val Arg Leu Gln Pro
 195 200 205
 Ser Glu Lys Phe Phe Tyr Ile Asp Gly Asn Glu Asn Phe His Val Ser
 210 215 220
 Ile Thr Ala Arg Tyr Leu Tyr Gly Glu Glu Val Glu Gly Val Ala Phe
 225 230 235 240
 Val Leu Phe Gly Val Lys Ile Asp Asp Ala Lys Lys Ser Ile Pro Asp
 245 250 255
 Ser Leu Thr Arg Ile Pro Ile Ile Asp Gly Asp Gly Lys Ala Thr Leu
 260 265 270
 Lys Arg Asp Thr Phe Arg Ser Arg Phe Pro Asn Leu Asn Glu Leu Val
 275 280 285
 Gly His Thr Leu Tyr Ala Ser Val Thr Val Met Thr Glu Ser Gly Ser
 290 295 300
 Asp Met Val Val Thr Glu Gln Ser Gly Ile His Ile Val Ala Ser Pro
 305 310 315 320
 Tyr Gln Ile His Phe Thr Lys Thr Pro Lys Tyr Phe Lys Pro Gly Met
 325 330 335
 Pro Tyr Glu Leu Thr Val Tyr Val Thr Asn Pro Asp Gly Ser Pro Ala
 340 345 350
 Ala His Val Pro Val Val Ser Glu Ala Phe His Ser Met Gly Thr Thr
 355 360 365
 Leu Ser Asp Gly Thr Ala Lys Leu Ile Leu Asn Ile Pro Leu Asn Ala
 370 375 380
 Gln Ser Leu Pro Ile Thr Val Arg Thr Asn His Gly Asp Leu Pro Arg
 385 390 395 400
 Glu Arg Gln Ala Thr Lys Ser Met Thr Ala Ile Ala Tyr Gln Thr Gln
 405 410 415
 Gly Gly Ser Gly Asn Tyr Leu His Val Ala Ile Thr Ser Thr Glu Ile
 420 425 430
 Lys Pro Gly Asp Asn Leu Pro Val Asn Phe Asn Val Lys Gly Asn Ala
 435 440 445
 Asn Ser Leu Lys Gln Ile Lys Tyr Phe Thr Tyr Leu Ile Leu Asn Lys
 450 455 460
 Gly Lys Ile Phe Lys Val Gly Arg Gln Pro Arg Arg Asp Gly Gln Asn
 465 470 475 480
 Leu Val Thr Met Asn Leu His Ile Thr Pro Asp Leu Ile Pro Ser Phe
 485 490 495
 Arg Phe Val Ala Tyr Tyr Gln Val Gly Asn Asn Glu Ile Val Ala Asp
 500 505 510
 Ser Val Trp Val Asp Val Lys Asp Thr Cys Met Gly Thr Leu Val Val
 515 520 525
 Lys Gly Asp Asn Leu Ile Gln Met Pro Gly Ala Ala Met Lys Ile Lys

530	535	540
Leu Glu Gly Asp Pro Gly Ala Arg Val Gly Leu Val Ala Val Asp Lys		
545	550	555
Ala Val Tyr Val Leu Asn Asp Lys Tyr Lys Ile Ser Gln Ala Lys Ile		
565	570	575
Trp Asp Thr Ile Glu Lys Ser Asp Phe Gly Cys Thr Ala Gly Ser Gly		
580	585	590
Gln Asn Asn Leu Gly Val Phe Glu Asp Ala Gly Leu Ala Leu Thr Thr		
595	600	605
Ser Thr Asn Leu Asn Thr Lys Gln Arg Ser Ala Ala Lys Cys Pro Gln		
610	615	620
Pro Ala Asn Arg Arg Arg Ser Ser Val Leu Leu Leu Asp Ser Asn		
625	630	635
Ala Ser Lys Ala Ala Glu Phe Gln Asp Gln Asp Leu Arg Lys Cys Cys		
645	650	655
Glu Asp Val Met His Glu Asn Pro Met Gly Tyr Thr Cys Glu Lys Arg		
660	665	670
Ala Lys Tyr Ile Gln Glu Gly Asp Ala Cys Lys Ala Ala Phe Leu Glu		
675	680	685
Cys Cys Arg Tyr Ile Lys Gly Val Arg Asp Glu Asn Gln Arg Glu Ser		
690	695	700
Glu Leu Phe Leu Ala Arg Asp Asp Asn Glu Asp Gly Phe Ile Ala Asp		
705	710	715
Ser Asp Ile Ile Ser Arg Ser Asp Phe Pro Lys Ser Trp Leu Trp Leu		
725	730	735
Thr Lys Asp Leu Thr Glu Glu Pro Asn Ser Gln Gly Ile Ser Ser Lys		
740	745	750
Thr Met Ser Phe Tyr Leu Arg Asp Ser Ile Thr Thr Trp Val Val Leu		
755	760	765
Ala Val Ser Phe Thr Pro Thr Lys Gly Ile Cys Val Ala Glu Pro Tyr		
770	775	780
Glu Ile Arg Val Met Lys Val Phe Phe Ile Asp Leu Gln Met Pro Tyr		
785	790	795
Ser Val Val Lys Asn Glu Gln Val Glu Ile Arg Ala Ile Leu His Asn		
805	810	815
Tyr Val Asn Glu Asp Ile Tyr Val Arg Val Glu Leu Leu Tyr Asn Pro		
820	825	830
Ala Phe Cys Ser Ala Ser Thr Lys Gly Gln Arg Tyr Arg Gln Gln Phe		
835	840	845
Pro Ile Lys Ala Leu Ser Ser Arg Ala Val Pro Phe Val Ile Val Pro		
850	855	860
Leu Glu Gln Gly Leu His Asp Val Glu Ile Lys Ala Ser Val Gln Glu		
865	870	875
Ala Leu Trp Ser Asp Gly Val Arg Lys Lys Leu Lys Val Val Pro Glu		
885	890	895
Gly Val Gln Lys Ser Ile Val Thr Ile Val Lys Leu Asp Pro Arg Ala		
900	905	910
Lys Gly Val Gly Gly Thr Gln Leu Glu Val Ile Lys Ala Arg Lys Leu		
915	920	925
Asp Asp Arg Val Pro Asp Thr Glu Ile Glu Thr Lys Ile Ile Ile Gln		
930	935	940
Gly Asp Pro Val Ala Gln Ile Ile Glu Asn Ser Ile Asp Gly Ser Lys		
945	950	955
Leu Asn His Leu Ile Ile Thr Pro Ser Gly Cys Gly Glu Gln Asn Met		
965	970	975
Ile Arg Met Ala Ala Pro Val Ile Ala Thr Tyr Tyr Leu Asp Thr Thr		
980	985	990
Glu Gln Trp Glu Thr Leu Gly Ile Asn Arg Arg Thr Glu Ala Val Asn		
995	1000	1005
Gln Ile Val Thr Gly Tyr Ala Gln Gln Met Val Tyr Lys Lys Ala Asp		

1010	1015	1020
His Ser Tyr Ala Ala Phe Thr Asn Arg Ala Ser Ser Ser Trp Leu Thr		
1025	1030	1035
Ala Tyr Val Val Lys Val Phe Ala Met Ala Ala Lys Met Val Ala Gly		1040
1045	1050	1055
Ile Ser His Glu Ile Ile Cys Gly Gly Val Arg Trp Leu Ile Leu Asn		
1060	1065	1070
Arg Gln Gln Pro Asp Gly Ala Phe Lys Glu Asn Ala Pro Val Leu Ser		
1075	1080	1085
Gly Thr Met Gln Gly Gly Ile Gln Gly Ala Glu Glu Val Tyr Leu		
1090	1095	1100
Thr Ala Phe Ile Leu Val Ala Leu Leu Glu Ser Lys Thr Ile Cys Asn		
1105	1110	1115
Asp Tyr Val Asn Ser Leu Asp Ser Ser Ile Lys Lys Ala Thr Asn Tyr		1120
1125	1130	1135
Leu Leu Lys Lys Tyr Glu Lys Leu Gln Arg Pro Tyr Thr Ala Leu		
1140	1145	1150
Thr Ala Tyr Ala Leu Ala Ala Asp Gln Leu Asn Asp Asp Arg Val		
1155	1160	1165
Leu Met Ala Ala Ser Thr Gly Arg Asp His Trp Glu Glu Tyr Asn Ala		
1170	1175	1180
His Thr His Asn Ile Glu Gly Thr Ser Tyr Ala Leu Leu Ala Leu		
1185	1190	1195
Lys Met Lys Lys Phe Asp Gln Thr Gly Pro Ile Val Arg Trp Leu Thr		1200
1205	1210	1215
Asp Gln Asn Phe Tyr Gly Glu Thr Tyr Gly Gln Thr Gln Ala Thr Val		
1220	1225	1230
Met Ala Phe Gln Ala Leu Ala Glu Tyr Glu Ile Gln Met Pro Thr His		
1235	1240	1245
Lys Asp Leu Asn Leu Asp Ile Thr Ile Glu Leu Pro Asp Arg Glu Val		
1250	1255	1260
Pro Ile Arg Tyr Arg Ile Asn Tyr Glu Asn Ala Leu Leu Ala Arg Thr		
1265	1270	1275
Val Glu Thr Lys Leu Asn Gln Asp Ile Thr Val Thr Ala Ser Gly Asp		1280
1285	1290	1295
Gly Lys Ala Thr Met Thr Ile Leu Thr Phe Tyr Asn Ala Gln Leu Gln		
1300	1305	1310
Glu Lys Ala Asn Val Cys Asn Lys Phe His Leu Asn Val Ser Val Glu		
1315	1320	1325
Asn Ile His Leu Asn Ala Met Gly Ala Lys Gly Ala Leu Met Leu Lys		
1330	1335	1340
Ile Cys Thr Arg Tyr Leu Gly Glu Val Asp Ser Thr Met Thr Ile Ile		
1345	1350	1355
Asp Ile Ser Met Leu Thr Gly Phe Leu Pro Asp Ala Glu Asp Leu Thr		1360
1365	1370	1375
Arg Leu Ser Lys Gly Val Asp Arg Tyr Ile Ser Arg Tyr Glu Val Asp		
1380	1385	1390
Asn Asn Met Ala Gln Lys Val Ala Val Ile Ile Tyr Leu Asn Lys Val		
1395	1400	1405
Ser His Ser Glu Asp Glu Cys Leu His Phe Lys Ile Leu Lys His Phe		
1410	1415	1420
Glu Val Gly Phe Ile Gln Pro Gly Ser Val Lys Val Tyr Ser Tyr Tyr		
1425	1430	1435
Asn Leu Asp Glu Lys Cys Thr Lys Phe Tyr His Pro Asp Lys Gly Thr		1440
1445	1450	1455
Gly Leu Leu Asn Lys Ile Cys Ile Gly Asn Val Cys Arg Cys Ala Gly		
1460	1465	1470
Glu Thr Cys Ser Ser Leu Asn His Gln Glu Arg Ile Asp Val Pro Leu		
1475	1480	1485
Gln Ile Glu Lys Ala Cys Glu Thr Asn Val Asp Tyr Val Tyr Lys Thr		

1490	1495	1500
Lys Leu Leu Arg Ile Glu Glu Gln Asp Gly Asn Asp Ile Tyr Val Met		
1505	1510	1515
Asp Val Leu Glu Val Ile Lys Gln Gly Thr Asp Glu Asn Pro Arg Ala		
1525	1530	1535
Lys Thr His Gln Tyr Ile Ser Gln Arg Lys Cys Gln Glu Ala Leu Asn		
1540	1545	1550
Leu Lys Val Asn Asp Asp Tyr Leu Ile Trp Gly Ser Arg Ser Asp Leu		
1555	1560	1565
Leu Pro Thr Lys Asp Lys Ile Ser Tyr Ile Ile Thr Lys Asn Thr Trp		
1570	1575	1580
Ile Glu Arg Trp Pro His Glu Asp Glu Cys Gln Glu Glu Phe Gln		
1585	1590	1595
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Gly Cys Pro Thr		
1620		

<210> 25

<211> 3039

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 25

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 gatgctgaaa atgaaattt gttcaaaaaaattt attccacttt gtaaagttat tcactgtcac 2100
 cctccaccag tgattgtcaa tgggaagcac acaggatga tggcagaaaa ctttctatat 2160
 gaaaaatgaag tctcttatga atgtgaccaa ggattctatc tcctggaga gaaaaaattt 2220
 cagtgcagaa gtgattctaa aggacatgga tcttgagcg ggccttcccc acagtgccta 2280
 cgatctcctc ctgtgactcg ctgcctaat ccagaagtca aacatggta caagctcaat 2340
 aaaacacatt ctgcatattc ccacaatgac atagtgtatg ttgactgcaa tcctggcttc 2400
 atcatgaatg gtatgcgcgt gattagggtt catactgata acacatgggt gccaggtgtg 2460
 ccaacttgta tgaaaaaagc cttcataggg tgcacaccctc cgcctaagac ccctaacggg 2520
 aaccataactg gtggaaacat agtcgattt tctctggaa tgtcaatcct gtacagctgt 2580
 gaccaaggct acctgctggt gggagaggca ctccctctt gcacacatga gggAACCTGG 2640
 agccaaacctg cccctcattt taaagaggtt aactgttagt caccagcaga tatggatgga 2700
 atccagaaag ggcttggacc aaggaaaatg tatcagttatg gagctgttgg 2760
 tgtgaagatg ggtatatgtt ggaaggcagt ccccagagcc agtgcctatc ggatccacaa 2820
 tggAACCTC cccttggcggt ttgcagatcc cgttctactt ctcctgttct ttgtggatt 2880
 gctgcaggtt tgatactt taccttctt attgtcattt ccttatacgt gatataaaaa 2940
 cacagagaac gcaattatta tacagatata agccagaaag aagctttca ttttagaagca 3000
 cgagaagttt attctgttga tccatataac ccagccagc 3039

<210> 26
 <211> 1033
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 26
 Met Gly Ala Ala Gly Leu Leu Gly Val Phe Leu Ala Leu Val Ala Pro
 1 5 10 15
 Gly Val Leu Gly Ile Ser Cys Gly Ser Pro Pro Pro Ile Leu Asn Gly
 20 25 30
 Arg Ile Ser Tyr Tyr Ser Thr Pro Ile Ala Val Gly Thr Val Ile Arg
 35 40 45
 Tyr Ser Cys Ser Gly Thr Phe Arg Leu Ile Gly Glu Lys Ser Leu Leu
 50 55 60
 Cys Ile Thr Lys Asp Lys Val Asp Gly Thr Trp Asp Lys Pro Ala Pro
 65 70 75 80
 Lys Cys Glu Tyr Phe Asn Lys Tyr Ser Ser Cys Pro Glu Pro Ile Val
 85 90 95
 Pro Gly Gly Tyr Lys Ile Arg Gly Ser Thr Pro Tyr Arg His Gly Asp
 100 105 110
 Ser Val Thr Phe Ala Cys Lys Thr Asn Phe Ser Met Asn Gly Asn Lys
 115 120 125
 Ser Val Trp Cys Gln Ala Asn Asn Met Trp Gly Pro Thr Arg Leu Pro
 130 135 140
 Thr Cys Val Ser Val Phe Pro Leu Glu Cys Pro Ala Leu Pro Met Ile
 145 150 155 160
 His Asn Gly His His Thr Ser Glu Asn Val Gly Ser Ile Ala Pro Gly
 165 170 175
 Leu Ser Val Thr Tyr Ser Cys Glu Ser Gly Tyr Leu Leu Val Gly Glu
 180 185 190
 Lys Ile Ile Asn Cys Leu Ser Ser Gly Lys Trp Ser Ala Val Pro Pro
 195 200 205
 Thr Cys Glu Glu Ala Arg Cys Lys Ser Leu Gly Arg Phe Pro Asn Gly
 210 215 220
 Lys Val Lys Glu Pro Pro Ile Leu Arg Val Gly Val Thr Ala Asn Phe
 225 230 235 240
 Phe Cys Asp Glu Gly Tyr Arg Leu Gln Gly Pro Pro Ser Ser Arg Cys

245	250	255
Val Ile Ala Gly Gln Gly Val Ala Trp Thr Lys Met Pro Val Cys Glu		
260	265	270
Glu Ile Phe Cys Pro Ser Pro Pro Pro Ile Leu Asn Gly Arg His Ile		
275	280	285
Gly Asn Ser Leu Ala Asn Val Ser Tyr Gly Ser Ile Val Thr Tyr Thr		
290	295	300
Cys Asp Pro Asp Pro Glu Glu Gly Val Asn Phe Ile Leu Ile Gly Glu		
305	310	315
Ser Thr Leu Arg Cys Thr Val Asp Ser Gln Lys Thr Gly Thr Trp Ser		
325	330	335
Gly Pro Ala Pro Arg Cys Glu Leu Ser Thr Ser Ala Val Gln Cys Pro		
340	345	350
His Pro Gln Ile Leu Arg Gly Arg Met Val Ser Gly Gln Lys Asp Arg		
355	360	365
Tyr Thr Tyr Asn Asp Thr Val Ile Phe Ala Cys Met Phe Gly Phe Thr		
370	375	380
Leu Lys Gly Ser Lys Gln Ile Arg Cys Asn Ala Gln Gly Thr Trp Glu		
385	390	395
Pro Ser Ala Pro Val Cys Glu Lys Glu Cys Gln Ala Pro Pro Asn Ile		
405	410	415
Leu Asn Gly Gln Lys Glu Asp Arg His Met Val Arg Phe Asp Pro Gly		
420	425	430
Thr Ser Ile Lys Tyr Ser Cys Asn Pro Gly Tyr Val Leu Val Gly Glu		
435	440	445
Glu Ser Ile Gln Cys Thr Ser Glu Gly Val Trp Thr Pro Pro Val Pro		
450	455	460
Gln Cys Lys Val Ala Ala Cys Glu Ala Thr Gly Arg Gln Leu Leu Thr		
465	470	475
Lys Pro Gln His Gln Phe Val Arg Pro Asp Val Asn Ser Ser Cys Gly		
485	490	495
Glu Gly Tyr Lys Leu Ser Gly Ser Val Tyr Gln Glu Cys Gln Gly Thr		
500	505	510
Ile Pro Trp Phe Met Glu Ile Arg Leu Cys Lys Glu Ile Thr Cys Pro		
515	520	525
Pro Pro Pro Val Ile Tyr Asn Gly Ala His Thr Gly Ser Ser Leu Glu		
530	535	540
Asp Phe Pro Tyr Gly Thr Thr Val Thr Tyr Thr Cys Asn Pro Gly Pro		
545	550	555
Glu Arg Gly Val Glu Phe Ser Leu Ile Gly Glu Ser Thr Ile Arg Cys		
565	570	575
Thr Ser Asn Asp Gln Glu Arg Gly Thr Trp Ser Gly Pro Ala Pro Leu		
580	585	590
Cys Lys Leu Ser Leu Leu Ala Val Gln Cys Ser His Val His Ile Ala		
595	600	605
Asn Gly Tyr Lys Ile Ser Gly Lys Glu Ala Pro Tyr Phe Tyr Asn Asp		
610	615	620
Thr Val Thr Phe Lys Cys Tyr Ser Gly Phe Thr Leu Lys Gly Ser Ser		
625	630	635
Gln Ile Arg Cys Lys Ala Asp Asn Thr Trp Asp Pro Glu Ile Pro Val		
645	650	655
Cys Glu Lys Glu Thr Cys Gln His Val Arg Gln Ser Leu Gln Glu Leu		
660	665	670
Pro Ala Gly Ser Arg Val Glu Leu Val Asn Thr Ser Cys Gln Asp Gly		
675	680	685
Tyr Gln Leu Thr Gly His Ala Tyr Gln Met Cys Gln Asp Ala Glu Asn		
690	695	700
Gly Ile Trp Phe Lys Lys Ile Pro Leu Cys Lys Val Ile His Cys His		
705	710	715
Pro Pro Pro Val Ile Val Asn Gly Lys His Thr Gly Met Met Ala Glu		
725	730	735

Asn Phe Leu Tyr Gly Asn Glu Val Ser Tyr Glu Cys Asp Gln Gly Phe
 740 745 750
 Tyr Leu Leu Gly Glu Lys Lys Leu Gln Cys Arg Ser Asp Ser Lys Gly
 755 760 765
 His Gly Ser Trp Ser Gly Pro Ser Pro Gln Cys Leu Arg Ser Pro Pro
 770 775 780
 Val Thr Arg Cys Pro Asn Pro Glu Val Lys His Gly Tyr Lys Leu Asn
 785 790 795 800
 Lys Thr His Ser Ala Tyr Ser His Asn Asp Ile Val Tyr Val Asp Cys
 805 810 815
 Asn Pro Gly Phe Ile Met Asn Gly Ser Arg Val Ile Arg Cys His Thr
 820 825 830
 Asp Asn Thr Trp Val Pro Gly Val Pro Thr Cys Met Lys Lys Ala Phe
 835 840 845
 Ile Gly Cys Pro Pro Pro Lys Thr Pro Asn Gly Asn His Thr Gly
 850 855 860
 Gly Asn Ile Ala Arg Phe Ser Pro Gly Met Ser Ile Leu Tyr Ser Cys
 865 870 875 880
 Asp Gln Gly Tyr Leu Leu Val Gly Glu Ala Leu Leu Leu Cys Thr His
 885 890 895
 Glu Gly Thr Trp Ser Gln Pro Ala Pro His Cys Lys Glu Val Asn Cys
 900 905 910
 Ser Ser Pro Ala Asp Met Asp Gly Ile Gln Lys Gly Leu Glu Pro Arg
 915 920 925
 Lys Met Tyr Gln Tyr Gly Ala Val Val Thr Leu Glu Cys Glu Asp Gly
 930 935 940
 Tyr Met Leu Glu Gly Ser Pro Gln Ser Gln Cys Gln Ser Asp His Gln
 945 950 955 960
 Trp Asn Pro Pro Leu Ala Val Cys Arg Ser Arg Ser Leu Ala Pro Val
 965 970 975
 Leu Cys Gly, Ile Ala Ala Gly Leu Ile Leu Leu Thr Phe Leu Ile Val
 980 985 990
 Ile Thr Leu Tyr Val Ile Ser Lys His Arg Glu Arg Asn Tyr Tyr Thr
 995 1000 1005
 Asp Thr Ser Gln Lys Glu Ala Phe His Leu Glu Ala Arg Glu Val Tyr
 1010 1015 1020
 Ser Val Asp Pro Tyr Asn Pro Ala Ser
 1025 1030

<210> 27
 <211> 3042
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 27
 atttcttgc accctcctcc tgaagtcaaa aatgctcgga aaccctatta ttcttcccc 60
 atagttcctg gaactgttct gaggtacact tgttcaccta gctaccgcct cattggagaa 120
 aaggctatct tttgtataag tgaaaatcaa gtgcacgcca cctgggataaa agctcctcct 180
 atatgtaat ctgtaaataa aaccattct tgctcagatc ccatagtgacc agggggattc 240
 atgaataaag gatctaaggc accattcaga catggtgatt ctgtgacatt tacctgtaaa 300
 gccaacttca ccatgaaagg aagcaaaact gtctggtgcc aggcaaatga aatgtgggga 360
 ccaacagtc tgccagtctg tgagagtgtat ttcctctgg agtgcctatc acttccaacg 420
 attcataatg gacaccacac aggacacat gttgaccagt ttgttgcgtgg gttgtctgtg 480
 acatacagtt gtgaacctgg ctatgttc actggaaaaa agacaatcaa gtgcttatct 540
 tcaggagact gggatggtgt catccccaca tgcaaagagg cccagtgta acatccagga 600
 aagttccca atggcaggt aaaggaacct ctgagcctc aggttggcac aactgtgtac 660

ttctcctgta atgaagggtta ccaattacaa ggacaaccct ctagtcagtg tgtaattgtt 720
 gaacagaaaag ccatctggac taagaagcca gtatgtaaag aaattctctg cccaccacct 780
 ccacaccttc gtaatggaa tcatacaggc agctttcag aaaatgtacc atatggaaac 840
 acagttaccc acacctgtga cccaaagccc gagaaaggcg tgagcttac tcttattgga 900
 gagaagacta tcaattgtac tactggtagt cagaagactg ggatctggag tggccctgct 960
 ccatattgtg tactttcaac ttctgcagtt ctgtgtttac aaccgaagat caaaagaggg 1020
 caaatattat ctatTTGAA agatagttat tcataataatg acactgtggc attttcttgt 1080
 gaacctgct tcaccttcaa gggcaacagg agcattcgat gcaatgctca tggcacatgg 1140
 gagccacccg taccagtgtg tgaaaaagga tgtagggctc ctcctaaaat tatcaatggg 1200
 caaaaagaag atagttactt gctcaactt gaccctggta catccataag atatagtgt 1260
 gaccctgct atttactggt gggagaggac actatacatt gcaccctgta gggaaagtgg 1320
 acacccatTA cTCCCCAGTG cacagtgtca gagtgtaaac cagtaggacc acatctctt 1380
 aagaggcctc agaatacgtt tattaggaca gctgttaatt cttctgtga tgaagggttc 1440

cagttaaatg agagtgcTTA tcaactgtgt caaggtacaa ttccTTGGTT tataaaaaatc 1500
 cgtcttGta aagaaaatcac ctgcccacca cttccTGTta tacacaacgg gacacataca 1560
 tggagttcct cagaagatgt cccatATGGA actgtggta catacatgtg ctatccTGGG 1620
 ccagaggaag gcgtaaaatt cAAACTCATC gggggagcaaa ccatccactg tacaagtgc 1680
 agcagagggaa gaggtccTGT gaggtagccT gctccTCTC gtaaaactttc cttcccaGCT 1740
 gtccAGTGCa cagacgttca tGTTGAAAAT ggagtcaAGC tcactgacAA taaAGCCCCA 1800
 tatttctaca atgatagtgt gatgttcaag tGtgatgtg gatataTTT gagtggaaAGC 1860
 agtcagatcc ggtgtaaAGC caataatacc tgggatcCTG aaaaaccact ttgtaaaaaaaa 1920
 gaaggatgtg agcctatgag agtacatggc cttccagatg attcacatAT aaaaactagtg 1980
 aaaagaacct gtcaaaatgg gtaccaggT actggatata cttatgagaa gttcaaaaat 2040
 gctgagaatg ggacttggTT taaaaagatt gaagtTTGta cagttattct ctgtcaacct 2100
 ccaccaaaaa ttgcaaatgg tggTCacaca ggcgtatgg caaagcactt cctatatggA 2160
 aatgaagttt cttatgaatg tGatgaaggg ttctatTTT tgggagagaa aagtTTGcag 2220
 tgcgtaaatg attctaaagg tcatggctc tggagtggac ctccaccaca atgcttacaa 2280
 tcttctcctc taactcatttccccgatcca gaagtcaaac atggttacAA actcaataaa 2340
 actcattctg cattttctca taatgacata gtacatTTT tctgcaatca aggcttcATC 2400
 atgaacggca gccacttgc aagggtgtcat actaataaca catggttacc aggtgtacca 2460
 acttgtatca gaaaggctc tttaggggtg cagtcTCCat ccacaatccc caatgggaat 2520
 catactggtg ggagtatAGC tcgattttcc cctggaaatgt cagtcatgtA cagtgcTAC 2580
 caaggctcc ttatggctgg agaggcacgt cttatctgtA ctcatgaggg tacTggagt 2640
 caacctcccc cttttgcaa agaggtaaAC tGtagcttc ctgaagatAC aaatggaaATC 2700
 cagaaggat ttcaacctgg gaaaaacctt cgattgggg ctactgtgac tctgaaatgt 2760
 gaggatgggt ataccttggA gggaaagtccc cagagccagt gcccaggatga cagccaatgg 2820
 aaccctccct tggcttttgc caaataccgt aggtggtaa ctattccTCT tatttgggt 2880
 atttctgtgg gctcagcact tATCATTGt atgagtgtcg gcttctgtat gatattaaaa 2940
 cacagagaaa gcaattatta tacaAAagaca agacccaaAG aaggagctc tcatTTAGAA 3000
 acacgagaag tatattctat tgatccatA aaccCAGCAA GC 3042

<210> 28
 <211> 1014
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 28
 Ile Ser Cys Asp Pro Pro Pro Glu Val Lys Asn Ala Arg Lys Pro Tyr
 1 5 10 15
 Tyr Ser Leu Pro Ile Val Pro Gly Thr Val Leu Arg Tyr Thr Cys Ser
 20 25 30
 Pro Ser Tyr Arg Leu Ile Gly Glu Lys Ala Ile Phe Cys Ile Ser Glu
 35 40 45
 Asn Gln Val His Ala Thr Trp Asp Lys Ala Pro Pro Ile Cys Glu Ser
 50 55 60
 Val Asn Lys Thr Ile Ser Cys Ser Asp Pro Ile Val Pro Gly Gly Phe

65	70	75	80
Met Asn Lys Gly Ser Lys Ala Pro Phe Arg His	Gly Asp Ser Val Thr		
85	90	95	
Phe Thr Cys Lys Ala Asn Phe Thr Met Lys	Gly Ser Lys Thr Val Trp		
100	105	110	
Cys Gln Ala Asn Glu Met Trp Gly Pro Thr Ala	Leu Pro Val Cys Glu		
115	120	125	
Ser Asp Phe Pro Leu Glu Cys Pro Ser Leu Pro	Thr Ile His Asn Gly		
130	135	140	
His His Thr Gly Gln His Val Asp Gln Phe	Val Ala Gly Leu Ser Val		
145	150	155	160
Thr Tyr Ser Cys Glu Pro Gly Tyr Leu Leu	Thr Gly Lys Lys Thr Ile		
165	170	175	
Lys Cys Leu Ser Ser Gly Asp Trp Asp Gly Val	Ile Pro Thr Cys Lys		
180	185	190	
Glu Ala Gln Cys Glu His Pro Gly Lys Phe	Pro Asn Gly Gln Val Lys		
195	200	205	
Glu Pro Leu Ser Leu Gln Val Gly Thr Thr	Val Tyr Phe Ser Cys Asn		
210	215	220	
Glu Gly Tyr Gln Leu Gln Gly Gln Pro Ser	Ser Gln Cys Val Ile Val		
225	230	235	240
Glu Gln Lys Ala Ile Trp Thr Lys Lys Pro	Val Cys Lys Glu Ile Leu		
245	250	255	
Cys Pro Pro Pro Pro Val Arg Asn Gly Ser	His Thr Gly Ser Phe		
260	265	270	
Ser Glu Asn Val Pro Tyr Gly Ser Thr Val	Thr Thr Tyr Thr Cys Asp Pro		
275	280	285	
Ser Pro Glu Lys Gly Val Ser Phe Thr Leu	Ile Gly Glu Lys Thr Ile		
290	295	300	
Asn Cys Thr Thr Gly Ser Gln Lys Thr Gly	Ile Trp Ser Gly Pro Ala		
305	310	315	320
Pro Tyr Cys Val Leu Ser Thr Ser Ala Val	Leu Cys Leu Gln Pro Lys		
325	330	335	
Ile Lys Arg Gly Gln Ile Leu Ser Ile Leu	Lys Asp Ser Tyr Ser Tyr		
340	345	350	
Asn Asp Thr Val Ala Phe Ser Cys Glu Pro	Gly Phe Thr Leu Lys Gly		
355	360	365	
Asn Arg Ser Ile Arg Cys Asn Ala His	Gly Thr Trp Glu Pro Pro Val		
370	375	380	
Pro Val Cys Glu Lys Gly Cys Gln Ala Pro	Pro Lys Ile Ile Asn Gly		
385	390	395	400
Gln Lys Glu Asp Ser Tyr Leu Leu Asn Phe	Asp Pro Gly Thr Ser Ile		
405	410	415	
Arg Tyr Ser Cys Asp Pro Gly Tyr Leu Leu	Val Gly Glu Asp Thr Ile		
420	425	430	
His Cys Thr Pro Glu Gly Lys Trp Thr Pro	Ile Thr Pro Gln Cys Thr		
435	440	445	
Val Ala Glu Cys Lys Pro Val Gly Pro His	Leu Phe Lys Arg Pro Gln		
450	455	460	
Asn Gln Phe Ile Arg Thr Ala Val Asn Ser	Ser Cys Asp Glu Gly Phe		
465	470	475	480
Gln Leu Ser Glu Ser Ala Tyr Gln Leu	Cys Gln Gly Thr Ile Pro Trp		
485	490	495	
Phe Ile Glu Ile Arg Leu Cys Lys Glu	Ile Thr Cys Pro Pro Pro Pro		
500	505	510	
Val Ile His Asn Gly Thr His Thr Trp Ser	Ser Ser Glu Asp Val Pro		
515	520	525	
Tyr Gly Thr Val Val Thr Tyr Met Cys Tyr	Pro Gly Pro Glu Glu Gly		
530	535	540	
Val Lys Phe Lys Leu Ile Gly Glu Gln Thr	Ile His Cys Thr Ser Asp		
545	550	555	560

Ser Arg Gly Arg Gly Ser Trp Ser Ser Pro Ala Pro Leu Cys Lys Leu
 565 570 575
 Ser Leu Pro Ala Val Gln Cys Thr Asp Val His Val Glu Asn Gly Val
 580 585 590
 Lys Leu Thr Asp Asn Lys Ala Pro Tyr Phe Tyr Asn Asp Ser Val Met
 595 600 605
 Phe Lys Cys Asp Asp Gly Tyr Ile Leu Ser Gly Ser Ser Gln Ile Arg
 610 615 620
 Cys Lys Ala Asn Asn Thr Trp Asp Pro Glu Lys Pro Leu Cys Lys Lys
 625 630 635 640
 Glu Gly Cys Glu Pro Met Arg Val His Gly Leu Pro Asp Asp Ser His
 645 650 655
 Ile Lys Leu Val Lys Arg Thr Cys Gln Asn Gly Tyr Gln Leu Thr Gly
 660 665 670
 Tyr Thr Tyr Glu Lys Cys Gln Asn Ala Glu Asn Gly Thr Trp Phe Lys
 675 680 685
 Lys Ile Glu Val Cys Thr Val Ile Leu Cys Gln Pro Pro Pro Lys Ile
 690 695 700
 Ala Asn Gly Gly His Thr Gly Met Met Ala Lys His Phe Leu Tyr Gly
 705 710 715 720
 Asn Glu Val Ser Tyr Glu Cys Asp Glu Gly Phe Tyr Leu Leu Gly Glu
 725 730 735
 Lys Ser Leu Gln Cys Val Asn Asp Ser Lys Gly His Gly Ser Trp Ser
 740 745 750
 Gly Pro Pro Pro Gln Cys Leu Gln Ser Ser Pro Leu Thr His Cys Pro
 755 760 765
 Asp Pro Glu Val Lys His Gly Tyr Lys Leu Asn Lys Thr His Ser Ala
 770 775 780
 Phe Ser His Asn Asp Ile Val His Phe Val Cys Asn Gln Gly Phe Ile
 785 790 795 800
 Met Asn Gly Ser His Leu Ile Arg Cys His Thr Asn Asn Thr Trp Leu
 805 810 815
 Pro Gly Val Pro Thr Cys Ile Arg Lys Ala Ser Leu Gly Cys Gln Ser
 820 825 830
 Pro Ser Thr Ile Pro Asn Gly Asn His Thr Gly Gly Ser Ile Ala Arg
 835 840 845
 Phe Pro Pro Gly Met Ser Val Met Tyr Ser Cys Tyr Gln Gly Phe Leu
 850 855 860
 Met Ala Gly Glu Ala Arg Leu Ile Cys Thr His Glu Gly Thr Trp Ser
 865 870 875 880
 Gln Pro Pro Pro Phe Cys Lys Glu Val Asn Cys Ser Phe Pro Glu Asp
 885 890 895
 Thr Asn Gly Ile Gln Lys Gly Phe Gln Pro Gly Lys Thr Tyr Arg Phe
 900 905 910
 Gly Ala Thr Val Thr Leu Glu Cys Glu Asp Gly Tyr Thr Leu Glu Gly
 915 920 925
 Ser Pro Gln Ser Gln Cys Gln Asp Asp Ser Gln Trp Asn Pro Pro Leu
 930 935 940
 Ala Leu Cys Lys Tyr Arg Arg Trp Ser Thr Ile Pro Leu Ile Cys Gly
 945 950 955 960
 Ile Ser Val Gly Ser Ala Leu Ile Ile Leu Met Ser Val Gly Phe Cys
 965 970 975
 Met Ile Leu Lys His Arg Glu Ser Asn Tyr Tyr Thr Lys Thr Arg Pro
 980 985 990
 Lys Glu Gly Ala Leu His Leu Glu Thr Arg Glu Val Tyr Ser Ile Asp
 995 1000 1005
 Pro Tyr Asn Pro Ala Ser
 1010

<211> 1033

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 29

Met Gly Ala Ala Gly Leu Leu Gly Val Phe Leu Ala Leu Val Ala Pro
1 5 10 15
Gly Val Leu Gly Ile Ser Cys Gly Ser Pro Pro Pro Val Leu Asn Gly
20 25 30
Arg Ile Ser Tyr Tyr Ser Thr Pro Ile Ala Val Gly Thr Val Ile Arg
35 40 45
Tyr Ser Cys Ser Gly Thr Phe Arg Leu Ile Gly Glu Lys Ser Leu Leu
50 55 60
Cys Ile Thr Lys Asp Lys Val Asp Gly Thr Trp Asp Lys Pro Ala Pro
65 70 75 80
Lys Cys Glu Tyr Phe Asn Lys Tyr Ser Ser Cys Pro Glu Pro Ile Val
85 90 95
Pro Gly Gly Tyr Lys Ile Arg Gly Ser Thr Pro Tyr Arg His Gly Asp
100 105 110
Ser Val Thr Phe Ala Cys Lys Thr Asn Phe Ser Met Asn Gly Asn Lys
115 120 125
Ser Val Trp Cys Gln Ala Asn Asn Met Trp Gly Pro Thr Arg Leu Pro
130 135 140
Thr Cys Val Ser Val Phe Pro Leu Glu Cys Pro Ala Leu Pro Met Ile
145 150 155 160
His Asn Gly His His Thr Ser Glu Asn Val Gly Ser Ile Ala Pro Gly
165 170 175
Leu Ser Val Thr Tyr Ser Cys Glu Ser Gly Tyr Leu Leu Val Gly Glu
180 185 190
Lys Ile Ile Asn Cys Leu Ser Ser Gly Lys Trp Ser Ala Val Pro Pro
195 200 205
Thr Cys Glu Glu Ala Arg Cys Lys Ser Leu Gly Arg Phe Pro Asn Gly
210 215 220
Lys Val Lys Glu Pro Pro Ile Leu Arg Val Gly Val Thr Ala Asn Phe
225 230 235 240
Phe Cys Asp Glu Gly Tyr Arg Leu Gln Gly Pro Pro Ser Ser Arg Cys
245 250 255
Val Ile Ala Gly Gln Gly Val Ala Trp Thr Lys Met Pro Val Cys Glu
260 265 270
Glu Ile Phe Cys Pro Ser Pro Pro Ile Leu Asn Gly Arg His Ile
275 280 285
Gly Asn Ser Leu Ala Asn Val Ser Tyr Gly Ser Ile Val Thr Tyr Thr
290 295 300
Cys Asp Pro Asp Pro Glu Glu Gly Val Asn Phe Ile Leu Ile Gly Glu
305 310 315 320
Ser Thr Leu Arg Cys Thr Val Asp Ser Gln Lys Thr Gly Thr Trp Ser
325 330 335
Gly Pro Ala Pro Arg Cys Glu Leu Ser Thr Ser Ala Val Gln Cys Pro
340 345 350
His Pro Gln Ile Leu Arg Gly Arg Met Val Ser Gly Gln Lys Asp Arg
355 360 365
Tyr Thr Tyr Asn Asp Thr Val Ile Phe Ala Cys Met Phe Gly Phe Thr
370 375 380
Leu Lys Gly Ser Lys Gln Ile Arg Cys Asn Ala Gln Gly Thr Trp Glu
385 390 395 400
Pro Ser Ala Pro Val Cys Glu Lys Glu Cys Gln Ala Pro Pro Asn Ile
405 410 415

Leu Asn Gly Gln Lys Glu Asp Arg His Met Val Arg Phe Asp Pro Gly
 420 425 430
 Thr Ser Ile Lys Tyr Ser Cys Asn Pro Gly Tyr Val Leu Val Gly Glu
 435 440 445
 Glu Ser Ile Gln Cys Thr Ser Glu Gly Val Trp Thr Pro Pro Val Pro
 450 455 460
 Gln Cys Lys Val Ala Ala Cys Glu Ala Thr Gly Arg Gln Leu Leu Thr
 465 470 475 480
 Lys Pro Gln His Gln Phe Val Arg Pro Asp Val Asn Ser Ser Cys Gly
 485 490 495
 Glu Gly Tyr Lys Leu Ser Gly Ser Val Tyr Gln Glu Cys Gln Gly Thr
 500 505 510
 Ile Pro Trp Phe Met Glu Ile Arg Leu Cys Lys Glu Ile Thr Cys Pro
 515 520 525
 Pro Pro Pro Val Ile Tyr Asn Gly Ala His Thr Gly Ser Ser Leu Glu
 530 535 540
 Asp Phe Pro Tyr Gly Thr Thr Val Thr Tyr Thr Cys Asn Pro Gly Pro
 545 550 555 560
 Glu Arg Gly Val Glu Phe Ser Leu Ile Gly Glu Ser Thr Ile Arg Cys
 565 570 575
 Thr Ser Asn Asp Gln Glu Arg Gly Thr Trp Ser Gly Pro Ala Pro Leu
 580 585 590
 Cys Lys Leu Ser Leu Leu Ala Val Gln Cys Ser His Val His Ile Ala
 595 600 605
 Asn Gly Tyr Lys Ile Ser Gly Lys Glu Ala Pro Tyr Phe Tyr Asn Asp
 610 615 620
 Thr Val Thr Phe Lys Cys Tyr Ser Gly Phe Thr Leu Lys Gly Ser Ser
 625 630 635 640
 Gln Ile Arg Cys Lys Ala Asp Asn Thr Trp Asp Pro Glu Ile Pro Val
 645 650 655
 Cys Glu Lys Glu Thr Cys Gln His Val Arg Gln Ser Leu Gln Glu Leu
 660 665 670
 Pro Ala Gly Ser Arg Val Glu Leu Val Asn Thr Ser Cys Gln Asp Gly
 675 680 685
 Tyr Gln Leu Thr Gly His Ala Tyr Gln Met Cys Gln Asp Ala Glu Asn
 690 695 700
 Gly Ile Trp Phe Lys Lys Ile Pro Leu Cys Lys Val Ile His Cys His
 705 710 715 720
 Pro Pro Pro Val Ile Val Asn Gly Lys His Thr Gly Met Met Ala Glu
 725 730 735
 Asn Phe Leu Tyr Gly Asn Glu Val Ser Tyr Glu Cys Asp Gln Gly Phe
 740 745 750
 Tyr Leu Leu Gly Glu Lys Lys Leu Gln Cys Arg Ser Asp Ser Lys Gly
 755 760 765
 His Gly Ser Trp Ser Gly Pro Ser Pro Gln Cys Leu Arg Ser Pro Pro
 770 775 780
 Val Thr Arg Cys Pro Asn Pro Glu Val Lys His Gly Tyr Lys Leu Asn
 785 790 795 800
 Lys Thr His Ser Ala Tyr Ser His Asn Asp Ile Val Tyr Val Asp Cys
 805 810 815
 Asn Pro Gly Phe Ile Met Asn Gly Ser Arg Val Ile Arg Cys His Thr
 820 825 830
 Asp Asn Thr Trp Val Pro Gly Val Pro Thr Cys Met Lys Lys Ala Phe
 835 840 845
 Ile Gly Cys Pro Pro Pro Pro Lys Thr Pro Asn Gly Asn His Thr Gly
 850 855 860
 Gly Asn Ile Ala Arg Phe Ser Pro Gly Met Ser Ile Leu Tyr Ser Cys
 865 870 875 880
 Asp Gln Gly Tyr Leu Leu Val Gly Glu Ala Leu Leu Leu Cys Thr His
 885 890 895
 Glu Gly Thr Trp Ser Gln Pro Ala Pro His Cys Lys Glu Val Asn Cys

900	905	910
Ser Ser Pro Ala Asp Met Asp Gly Ile Gln Lys Gly Leu Glu Pro Arg		
915	920	925
Lys Met Tyr Gln Tyr Gly Ala Val Val Thr Leu Glu Cys Glu Asp Gly		
930	935	940
Tyr Met Leu Glu Gly Ser Pro Gln Ser Gln Cys Gln Ser Asp His Gln		
945	950	955
		960
Trp Asn Pro Pro Leu Ala Val Cys Arg Ser Arg Ser Leu Ala Pro Val		
965	970	975
Leu Cys Gly Ile Ala Ala Gly Leu Ile Leu Leu Thr Phe Leu Ile Val		
980	985	990
Ile Thr Leu Tyr Val Ile Ser Lys His Arg Glu Arg Asn Tyr Tyr Thr		
995	1000	1005
Asp Thr Ser Gln Lys Glu Ala Phe His Leu Glu Ala Arg Glu Val Tyr		
1010	1015	1020
Ser Val Asp Pro Tyr Asn Pro Ala Ser		
1025	1030	